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International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 :
C12N 15/12, C07K 14/705, C12N 5/10, 15/57, 9/48, 9/14, 15/55

A2

(11) International Publication Number: WO 98/21328

(43) International Publication Date: 22 May 1998 (22.05.98)

(21) International Application Number: PCT/JP97/04056

(22) International Filing Date: 7 November 1997 (07.11.97)

(30) Priority Data:
8/301429 13 November 1996 (13.11.96) JP

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(81) Designated States: AU, CA, JP, MX, US, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).

Published
Without international search report and to be republished upon receipt of that report.

(54) Title: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNAS ENCODING THESE PROTEINS

(57) Abstract

Proteins containing any of the amino acid sequences represented by Sequence No. 1 to Sequence No. 2 or by Sequence No. 4 to Sequence No. 25 and DNAs encoding said proteins exemplified by cDNAs containing any of the base sequences represented by Sequence No. 26 to Sequence No. 50. Said proteins can be provided by expressing cDNAs encoding human proteins having transmembrane domains and recombinants of these human cDNAs.

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DESCRIPTION

Human Proteins Having Transmembrane Domains and DNAs Encoding These Proteins

TECHINICAL FIELD

The present invention relates to human proteins having transmembrane domains, DNAs encoding these proteins and eukaryotic cells expressing those DNAs. The proteins of the present invention can be used as pharmaceuticals or as antigens for preparing antibodies against said proteins. The cDNAs of the present invention can be used as probes for the gene diagnosis and gene sources for the gene therapy. Furthermore, the cDNAs can be used as gene sources for large-scale production of the proteins encoded by said cDNAs. Moreover, the cells introduced with DNAs encoding trans-membrane proteins therein and expressing transmembrane proteins in large amounts can be used for detection of the corresponding ligands as well as screening of novel low molecular medicines.

BACKGROUND ART

Membrane proteins play important roles, as signal receptors, ion channels, transporters, etc., for the material transportation and the information transmission which are mediated by the cell membrane. Their examples include receptors for a variety of cytokines, ion channels for the sodium ion, the potassium ion, the chloride ion, etc., transporters for saccharides and amino acids, and so on,

where the genes for many of them have been cloned already.

It has been clarified that the abnormalities of these membrane proteins are related to a number of hitherto cryptogenic diseases. For example, a gene for a membrane protein having 12 transmembrane domains was identified as the gene responsible for cystic fibrosis [Rommens, J. M. et al., Science 245: 1059-1065 (1989)]. In addition, it has been clarified that several membrane proteins act as the receptors when a virus infects the cells. For example, HIV-1 is revealed to infect into the cells through the mediation of a membrane protein fusin, a membrane protein on the T-cell membrane, having a CD-4 antigen and 7 transmembrane domains [Feng, Y. et al., Science 272: 872-877 (1996)]. Therefore, discovery of a new membrane protein is anticipated to lead to the elucidation of the causes of many diseases, whereby isolation of a new gene coding for the membrane protein has been desired.

Heretofore, owing to difficulty in the purification, many of membrane proteins have been isolated by an approach from the gene side. A general method is the so-called expression cloning which comprises transfection of a cDNA library in the animal cells to express the cDNA and then detection of the cells expressing the target membrane protein on the membrane by an immunological technique using an antibody or a biological technique for the change in the membrane permeability. However, this method is applicable only to cloning of a gene for a membrane protein with a known function.

In general, membrane proteins possess hydrophobic

transmembrane domains inside the proteins which are synthesized in the ribosome and then remain in the phospholipid to be trapped in the membrane. Accordingly, the evidence of the cDNA for encoding the membrane protein is provided by determination of the whole base sequence of a full-length cDNA followed by detection of highly hydrophobic transmembrane domains in the amino acid sequence of the protein encoded by said cDNA.

The object of the present invention is to provide novel human proteins having transmembrane domains, DNAs encoding said proteins and transformed eukaryotic cells capable of expressing said DNAs.

As the result of intensive studies, the present inventors were successful in cloning of cDNAs having transmembrane domains from a human full-length cDNA bank, thereby completing the present invention. That is to say, the present invention provides proteins containing any of the amino acid sequences represented by Sequence No. 1 to Sequence No. 2 or by Sequence No. 4 to Sequence No. 25 that are human proteins having transmembrane domains. The present invention also provides DNAs encoding said proteins such as cDNAs containing any of the base sequences represented by Sequence No. 26 to Sequence No. 50 and transformed eukaryotic cells capable of expressing said DNAs.

Each of the proteins of the present invention can be obtained, for example, by a method for isolation from human organs, cell lines, etc, a method for preparation of the peptide by the chemical synthesis on the basis of the amino acid sequence of the present invention, or a method for

production with the recombinant DNA technology using the DNA encoding the transmembrane domains of the present invention, wherein the method for obtainment by the recombinant DNA technology is employed preferably. For example, an in vitro expression can be achieved by preparation of an RNA by the in vitro transcription from a vector having a cDNA of the present invention, followed by the in vitro translation using this RNA as a template. Also, the recombination of the translation domain to a suitable expression vector by the method known in the art leads to the expression of a large amount of the encoded protein by using prokaryotic cells (e.g. *Escherichia coli, Bacillus subtilis)* or eukaryotic cells (e.g. yeasts, insect cells, animal cells).

In the case in which a protein of the present invention is expressed by a microorganism such as *Escherichia coli*, the translation region of a cDNA of the present invention is constructed in an expression vector having an origin, a promoter, ribosome-binding site(s), cDNA-cloning site(s), a terminator, etc. that can be replicated in the microorganism and, after transformation of the host cells with said expression vector, the thus-obtained transformant is incubated, whereby the protein encoded by said cDNA can be produced on a large scale in the microorganism. In that case, a protein fragment containing an optional region can be obtained by performing the expression with inserting an initiation codon and a termination codon before and after the optional translation region. Alternatively, a fusion protein with another protein can be expressed. Only a protein portion encoding said cDNA can be obtained by cleavage of said fusion

protein with an appropriate protease.

In the case wherein a protein of the present invention is to be produced in eukaryotic cells, the translation region of said cDNA may be subjected to recombination to an expression vector for eukaryotic cells having a promoter, a splicing domain, a poly(A) addition site, etc. and transfected into the eukaryotic cells so that the protein is produced as a membrane protein on the cell membrane surface. As the expression vector, there are exemplified pKA1, pCDM8, pSVK3, pMSG, pSVL, pBK-CMV, pBK-RSV, EBV vector, pRS, pYES2, etc. Examples of the eukaryotic cells are mamamlian animal culture cells (e.g. simian renal cells COS7, chinese hamster ovarian cells CHO), blast yeasts, fission yeasts, silkworm yeasts, South African clawed toad oocytes, etc. However, any eukaryotic cells may be used insofar as the protein of the invention can be expressed on the cell membrane surface. In order to introduce the expression vector into the eukaryotic cells, there may be used any per se conventional method such as electroporation method, calcium phosphate method, liposome method or DEAE dextran method.

For separation and purification of the protein of the invention from the culture after expression of such protein in prokaryotic cells or eukaryotic cells, conventional separation operations may be adopted, if necessary, in their proper combinaion. Examples of the conventional separation operations are treatment with a denaturing agent (e.g. urea) or a surfactant, ultrasonic treatment, enzymatic digestion, salting out, solvent precipitation, dialysis, centrifugation, ultrafiltration, gel filtration, SDS-PAGE, isoelectric point

electrophoresis, ion exchange chromatography, hydrophobic chromatography, affinity chromatography, reverse phase chromatography, etc.

The proteins of the present invention include peptide fragments (more than 5 amino acid residues) containing any partial amino acid sequence of the amino acid sequences represented by Sequence No. 1 to Sequence No. 2 or by Sequence No. 4 to Sequence No. 25. These fragments can be used as antigens for preparation of the antibodies. Also, the proteins of the present invention that have signal sequences appear in the form of maturation proteins on the cell surface, after the signal sequences are removed. Therefore, these maturation proteins shall come within the scope of the present invention. The N-terminal amino acid sequences of the maturation proteins can be easily identified by using the method for the cleavage-site determination in a signal sequence [Japanese Patent Kokai Publication No. 1996-187100]. Furthermore, many membrane proteins are subjected to the processing on the cell surface to be converted to the secretor forms. These secretor proteins or peptides shall come within the scope of the present invention. When glycosylation sites are present in the amino acid sequences, expression in appropriate animal cells affords glycosylated proteins. Therefore, these glycosylated proteins or peptides also shall come within the scope of the present invention.

The DNAs of the present invention include all DNAs encoding the above-mentioned proteins. Said DNAs can be obtained using the method by chemical synthesis, the method by cDNA cloning, and so on.

Each of the cDNAs of the present invention can be cloned from, for example, a cDNA library of the human cell origin. The cDNA is synthesized using as a template a poly(A)$^+$ RNA extracted from human cells. The human cells may be cells delivered from the human body, for example, by the operation or may be the culture cells. The cDNA can be synthesized by using any method selected from the Okayama-Berg method [Okayama, H. and Berg, P., Mol. Cell. Biol. 2: 161-170 (1982)], the Gubler-Hoffman method [Gubler, U. and Hoffman, J. Gene 25: 263-269 (1983)], and so on, but it is preferred to use the capping method [Kato, S. et al., Gene 150: 243-250 (1994)] as illustrated in Examples in order to obtain a full-length clone in an effective manner.

The primary selection of a cDNA encoding a human protein having transmembrane domain(s) is performed by the sequencing of a partial base sequence of the cDNA clone selected at random from the cDNA library, sequencing of the amino acid sequence encoded by the base sequence, and recognition of the presence or absence of hydrophobic site(s) in the resulting N-terminal amino acid sequence region. Next, the secondary selection is carried out by determination of the whole base sequence by the sequencing and the protein expression by the in vitro translation. The ascertainment of the cDNA of the present invention for encoding the protein having the secretory signal sequence is performed by using the signal sequence detection method [Yokoyama-Kobayashi, M. et al., Gene 163: 193-196 (1995)]. In other words, the ascertainment for the coding portion of the inserted cDNA fragment to function as a signal sequence is provided by

fusing a cDNA fragment encoding the N-terminus of the target protein with a cDNA encoding the protease domain of urokinase and then expressing the resulting cDNA in COS7 cells to detect the urokinase activity in the cell culture medium. On the other hand, the N-terminal region is judged to remain in the membrane in the case where the urokinase activity is not detected in the cell culture medium.

The cDNAs of the present invention are characterized by containing any of the base sequences represented by Sequence No. 26 to Sequence No. 50 and any of the base sequences represented by Sequence No. 51 to Sequence No. 75. Table 1 summarizes the clone number (HP number), the cells affording the cDNA, the total base number of the cDNA, and the number of the amino acid residues of the encoded protein, for each of the cDNAs.

Table 1

Sequence Number	HP Number	Cells	Number of Bases	Number of Amino Acid Residues
1, 26, 51	HP00442	HT-1080	986	205
2, 27, 52	HP00804	Leucocyte	1824	371
3, 28, 53	HP01098	Stomach cancer	1076	179
4, 29, 54	HP01148	Liver	1591	347
5, 30, 55	HP01293	Liver	1888	554
6, 31, 56	HP10013	KB	2033	350
7, 32, 57	HP10034	HT-1080	911	209
8, 33, 58	HP10050	HT-1080	601	163

9, 34, 59	HP10071	Stomach cancer	394	92
10, 35, 60	HP10076	U937	732	172
11, 36, 61	HP10085	U937	697	149
12, 37, 62	HP10122	Stomach cancer	1186	188
13, 38, 63	HP10136	U937	1409	215
14, 40, 64	HP10175	Stomach cancer	974	112
15, 41, 65	HP10179	KB	925	114
16, 41, 66	HP10196	HT-1080	1115	327
17, 42, 67	HP10235	HT-1080	1721	373
18, 43, 68	HP10297	Stomach cancer	1504	183
19, 44, 69	HP10299	Stomach cancer	532	116
20, 45, 70	HP10301	KB	662	152
21, 46, 71	HP10302	Liver	2373	559
22, 47, 72	HP10304	U-2 OS	1404	330
23, 48, 73	HP10305	U-2 OS	893	108
24, 49, 74	HP10306	U-2 OS	690	101
25, 50, 75	HP10328	KB	2186	372

Hereupon, the same clone as any of the cDNAs of the present invention can be easily obtained by screening of the cDNA library constructed from the cell line or the human tissue employed in the present invention, by the use of an oligonucleotide probe synthesized on the basis of the corresponding cDNA base sequence depicted in Sequence No. 51 to Sequence No. 75.

In general, the polymorphism due to the individual difference is frequently observed in human genes. Therefore, any cDNA that is subjected to insertion or deletion of one or plural nucleotides and/or substitution with other nucleotides in Sequence No. 51 to Sequence No. 75 shall come within the scope of the present invention.

In a similar manner, any protein that is produced by these modifications comprising insertion or deletion of one or plural nucleotides and/or substitution with other nucleotides shall come within the scope of the present invention, as far as said protein possesses the activity of the corresponding protein having the amino acid sequence represented by Sequence No. 1 to Sequence No. 2 or by Sequence No. 4 to Sequence No. 25.

The cDNAs of the present invention include cDNA fragments (more than 10 bp) containing any partial base sequence of the base sequence represented by Sequence No. 26 to No. 50 or of the base sequence represented by Sequence No. 51 to No. 75. Also, DNA fragments consisting of a sense chain and an anti-sense chain shall come within this scope. These DNA fragments can be used as the probes for the gene diagnosis.

BRIEF DESCRIPTION OF DRAWINGS

Figure 1: A figure depicting the structure of the secretory signal sequence detection vector pSSD3.

Figure 2: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP00442.

Figure 3: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP00804.

Figure 4: A figure showing the result on the northern-blot hybridization of clone HP00804.

Figure 5: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01098.

Figure 6: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01148.

Figure 7: A figure showing the result on the northern-blot hybridization of clone HP01148.

Figure 8: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01293.

Figure 9: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10013.

Figure 10: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10034.

Figure 11: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10050.

Figure 12: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10071.

Figure 13: A figure depicting the

hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10076.

Figure 14: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10085.

Figure 15: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10122.

Figure 16: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10136.

Figure 17: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10175.

Figure 18: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10179.

Figure 19: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10196.

Figure 20: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10235.

Figure 21: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10297.

Figure 22: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10299.

Figure 23: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10301.

Figure 24: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10302.

Figure 25: A figure depicting the hydrophobicity/hydrophil the protein encoded by clone HP10304.

Figure 26: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10305.

Figure 27: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10306.

Figure 28: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10328.

BEST MODE FOR CARRING OUT INVENTION

EXAMPLE

The present invention is embodied in more detail by the following examples, but this embodiment is not intended to restrict the present invention. The basic operations and the enzyme reactions with regard to the DNA recombination are carried out according to the literature [Molecular Cloning. A Laboratory Manual", Cold Spring Harbor Laboratory, 1989]. Unless otherwise stated, restrictive enzymes and a variety of modification enzymes to be used were those available from

TAKARA SHUZO. The manufacturer's instructions were used for the buffer compositions as well as for the reaction conditions, in each of the enzyme reactions. The cDNA synthesis was carried out according to the literature [Kato, S. et al., Gene 150: 243-250 (1994)].

(1) Preparation of Poly(A)$^+$ RNA

The fibrosarcoma cell line HT-1080 (ATCC CCL 121), the epidermoid carcinoma cell line KB (ATCC CRL 17), the histiocyte lymphoma cell line U937 (ATCC CRL 1593), the osterosarcoma U-2 OS (ATCC HTB 96), a leukocyte isolated from the peripheral blood, tissues of stomach cancer delivered by the operation, and liver were used for human cells to extract mRNAs. Each of the cell lines was cultured by a conventional procedure.

After about 1 g of human tissues was homogenized in 20 ml of a 5.5 M guanidinium thiocyanate solution, total mRNAs were prepared in accordance with the literature [Okayama, H. et al., "Methods in Enzymology" Vol. 164, Academic Press, 1987]. These mRNAs were subjected to chromatography using an oligo(dT)-cellulose column washed with 20 mM Tris-hydrochloric acid buffer solution (pH 7.6), 0.5 M NaCl, and 1 mM EDTA to obtain a poly(A)$^+$ RNA in accordance with the above-mentioned literature.

(2) Construction of cDNA Library

To a solution of 10 μg of the above-mentioned poly(A)$^+$ RNA in 100 mM Tris-hydrochloric acid buffer solution (pH 8) was added one unit of an RNase-free, bacterium-origin alkaline phosphatase and the resulting solution was allowed to react at 37°C for one hour. After the reaction solution

underwent the phenol extraction followed by the ethanol precipitation, the obtained pellets were dissolved in a mixed solution of 50 mM sodium acetate (pH 6), 1 mM EDTA, 0.1% 2-mercaptoethanol, and 0.01% Triton X-100. Thereto was added one unit of a tobacco-origin pyrophosphatase (Epicenter Technologies) and the resulting solution at a total volume of 100 µl was allowed to react at 37°C for one hour. After the reaction solution underwent the phenol extraction followed by the ethanol precipitation, the thus-obtained pellets were dissolved in water to obtain a decapped poly(A)$^+$ RNA solution.

To a solution of the decapped poly(A)$^+$ RNA and 3 nmol of a DNA-RNA chimeric oligonucleotide (5'-dG-dG-dG-dG-dA-dA-dT-dT-dC-dG-dA-G-G-A-3') in a mixed aqueous solution of 50 mM Tris-hydrochloric acid buffer solution (pH 7.5), 0.5 mM ATP, 5 mM $MgCl_2$, 10 mM 2-mercaptoethanol, and 25% polyethylene glycol were added 50 units of T4 RNA ligase and the resulting solution at a total volume of 30 µl was allowed to react at 20°C for 12 hours. After the reaction solution underwent the phenol extraction followed by the ethanol precipitation, the thus-obtained pellets were dissolved in water to obtain a chimeric oligo-capped poly(A)$^+$ RNA.

After the vector pKA1 developed by the present inventors (Japanese Patent Kokai Publication No. 1992-117292) was digested with KpnI, an about 60-dT tail was inserted by a terminal transferase. This product was digested with EcoRV to remove the dT tail at one side and the resulting molecule was used as a vectorial primer.

After 6 µg of the previously-prepared chimeric oligo-

capped poly(A)$^+$ RNA was annealed with 1.2 μg of the vectorial primer, the product was dissolved in a mixed solution of 50 mM Tris-hydrochloric acid buffer solution (pH 8.3), 75 mM KCl, 3 mM $MgCl_2$, 10 mM dithiothreitol, and 1.25 mM dNTP (dATP + dCTP + dGTP + dTTP), mixed with 200 units of a reverse transferase (GIBCO-BRL), and the resulting solution at a total volume of 20 μl was allowed to react at 42°C for one hour. After the reaction solution underwent the phenol extraction followed by the ethanol precipitation, the thus-obtained pellets were dissolved in a mixed solution of 50 mM Tris-hydrochloric acid buffer solution (pH 7.5), 100 mM NaCl, 10 mM $MgCl_2$, and 1 mM dithiothreitol. Thereto were added 100 units of EcoRI and the resulting solution at a total volume of 20 μl was allowed to react at 37°C for one hour. After the reaction solution underwent the phenol extraction followed by the ethanol precipitation, the obtained pellets were dissolved in a mixed solution of 20 mM Tris-hydrochloric acid buffer solution (pH 7.5), 100 mM KCl, 4 mM $MgCl_2$, 10 mM $(NH_4)_2SO_4$, and 50 μg/ml bovine serum albumin. Thereto were added 60 units of *Escherichia coli* DNA ligase and the resulting solution was allowed to react at 16°C for 16 hours. To the reaction solution were added 2 μl of 2 mM dNTP, 4 units of *Escherichia coli* DNA polymerase I, and 0.1 unit of *Escherichia coli* DNase H and the resulting solution was allowed to react at 12°C for one hour and then at 22°C for one hour.

Next, the cDNA-synthesis reaction solution was used to transform *Escherichia coli* DH12S (GIBCO-BRL). The

transformation was carried out by the electroporation method. A portion of the transformant was inoculated on a 2xYT agar culture medium containing 100 μg/ml ampicillin, which was incubated at 37°C overnight. A colony grown on the culture medium was randomly picked up and inoculated on 2 ml of the 2xYT culture medium containing 100 μg/ml ampicillin, which was incubated at 37°C overnight. The culture medium was centrifuged to separate the cells, from which a plasmid DNA was prepared by the alkaline lysis method. After the plasmid DNA was double-digested with EcoRI and NotI, the product was subjected to 0.8% agarose gel electrophoresis to determine the size of the cDNA insert. In addition, by the use of the obtained plasmid as a template, the sequence reaction using M13 universal primer labeled with a fluorescent dye and Taq polymerase (a kit of Applied Biosystems Inc.) was carried out and the product was analyzed by a fluorescent DNA-sequencer (Applied Biosystems Inc.) to determine the base sequence of the cDNA 5'-terminal of about 400 bp. The sequence data were filed as a homo-protein cDNA bank data base.

(3) Selection of cDNAs Encoding Proteins Having Transmembrane Domains

The base sequence registered in the homo-protein cDNA bank was converted to three frames of amino acid sequences and the presence or absence of an open reading frame (ORF) beginning from the initiation codon. Then, the selection was made for the presence of a signal sequence that is characteristic to a secretory protein at the N-terminal of the portion encoded by ORF. These clones were sequenced from the both 5' and 3' directions by using the deletion method to

determine the whole base sequence. The hydrophobicity/hydrophilicity profiles were obtained for proteins encoded by ORF by the Kyte-Doolittle method [Kyte, J. & Doolittle, R. F., J. Mol. Bio. 157: 105-132 (1982)] to examine the presence or absence of a hydrophobic region. In the case in which there is a hydrophobic region of putative transmembrane domain(s) in the amino acid sequence of an encoded protein, this protein was considered as a membrane protein.

(4) Construction of Secretory Signal Detection Vector pSSD3

One microgram of pSSD1 carrying the SV40 promoter and a cDNA encoding the protease domain of urokinase [Yokoyama-Kobayashi, M. et al., Gene 163: 193-196 (1995)] was digested with 5 units of BglII and 5 units of EcoRV. Then, after dephosphorylation at the 5′ terminal by the CIP treatment, a DNA fragment of about 4.2 kbp was purified by cutting off from the gel of agarose gel electrophoresis.

Two oligo DNA linkers, L1 (5′-GATCCCGGGTCACGTGGGAT-3′) and L2 (5′-ATCCCACGTGACCCGG-3′), were synthesized and phosphorylated by T4 polynucleotide kinase. After annealing of the both linkers, followed by ligation with the previously-prepared pSSD1 fragment by T4 DNA ligase, *Escherichia coli* JM109 was transformed. A plasmid pSSD3 was prepared from the transformant and the objective recombinant was confirmed by the determination of the base sequence of the linker-inserted fragment. Figure 1 illustrates the structure of the thus-obtained plasmid. The present plasmid vector carries three types of blunt-end formation restriction enzyme sites, SmaI, PmaCI, and EcoRV. Since these cleavage

sites are positioned in succession at an interval of 7 bp, selection of an appropriate site in combination of three types of frames for the inserting cDNA allows to construct a vector expressing a fusion protein.

(5) Functional Verification of Secretory Signal Sequence

Whether the N-terminal hydrophobic region in the secretory protein clone candidate obtained in the above-mentioned steps functions as the secretory signal sequence was verified by the method described in the literature [Yokoyama-Kobayashi, M. et al., Gene 163: 193-196 (1995)]. First, the plasmid containing the target cDNA was cleaved at an appropriate restriction enzyme site that existed at the downstream of the portion expected for encoding the secretory signal sequence. In the case in which this restriction enzyme site was a protruding terminus, the site was blunt-ended by the Klenow treatment or treatment with the mung-bean nuclease. Digestion with HindIII was further carried out and a DNA fragment containing the SV40 promoter and a cDNA encoding the secretory sequence at the downstream of the promoter was separated by agarose gel electrophoresis. This fragment was inserted between the pSSD3 HindIII site and a restriction enzyme site selected so as to match with the urokinase-coding frame, thereby constructing a vector expressing a fusion protein of the secretory signal portion of the target cDNA and the urokinase protease domain.

After *Escherichia coli* (host: JM109) bearing the fusion-protein expression vector was incubated at 37°C for 2 hours in 2 ml of the 2xYT culture medium containing 100 μg/ml ampicillin, the helper phage M13KO7 (50 μl) was added and the

incubation was continued at 37°C overnight. A supernatant separated by centrifugation underwent precipitation with polyethylene glycol to obtain single-stranded phage particles. These particles were suspended in 100 µl of 1 mM Tris-0.1 mM EDTA, pH 8 (TE). Also, there was used as a control a suspension of single-stranded particles prepared in the same manner from the vector pKA1-UPA containing pSSD3 and a full-length cDNA of urokinase [Yokoyama-Kobayashi, M. et al., Gene 163: 193-196 (1995)].

The simian-kidney-origin culture cells, COS7, were incubated at 37°C in the presence of 5% CO_2 in the Dulbecco's modified Eagle's culture medium (DMEM) containing 10% fetal calf albumin. Into a 6-well plate (Nunc Inc., 3 cm in the well diameter) were inoculated 1×10^5 COS7 cells and incubation was carried out at 37°C for 22 hours in the presence of 5% CO_2. After the culture medium was removed, the cell surface was washed with a phosphate buffer solution and then washed again with DMEM containing 50 mM Tris-hydrochloric acid (pH 7.5) (TDMEM). To the cells were added 1 µl of the single-stranded phage suspension, 0.6 ml of the DMEM culture medium, and 3 µl of TRANSFECTAM™ (IBF Inc.) and the resulting mixture was incubated at 37°C for 3 hours in the presence of 5% CO_2. After the sample solution was removed, the cell surface was washed with TDMEM, 2 ml per well of DMEM containing 10% fetal calf albumin was added, and the incubation was carried out at 37°C for 2 days in the presence of 5% CO_2.

To 10 ml of 50 mM phosphate buffer solution (pH 7.4)

containing 2% bovine fibrinogen (Miles Inc.), 0.5% agarose, and 1 mM potassium chloride were added 10 units of human thrombin (Mochida Pharmaceutical Co., Ltd.) and the resulting mixture was solidified in a plate of 9 cm in diameter to prepare a fibrin plate. Ten microliters of the culture supernatant of the transfected COS7 cells were spotted on the fibrin plate, which was incubated at 37°C for 15 hours. The diameter of the thus-obtained clear circle was taken as an index for the urokinase activity. In the case in which a cDNA fragment codes for the amino acid sequence that functions as a secretory signal sequence, a fusion protein is secreted to form a clear circle by its urokinase activity. Therefore, in the case in which a clear circle is not formed, the fusion protein remains as trapped in the membrane and the cDNA fragment is considered to code for a transmembrane domain.

(6) Protein Synthesis by In Vitro Translation

The plasmid vector carrying the cDNA of the present invention was utilized for the in vitro transcription/translation by the T_NT rabbit reticulocyte lysate kit (Promega Biotec). In this case, [^{35}S]methionine was added and the expression product was labeled with the radioisotope. All reactions were carried out by following the protocols attached to the kit. Two micrograms of the plasmid was allowed to react at 30°C for 90 minutes in total 25 ml of a reaction solution containing 12.5 µl of the T_NT rabbit reticulocyte lysate, 0.5 µl of the buffer solution (attached to the kit), 2 µl of an amino acid mixture (methionine-free), 2 µl (0.37 MBq/µl) of [^{35}S]methionine (Amersham Corporation), 0.5 µl of T7 RNA polymerase, and 20 U of RNasin. To 3 µl of

the reaction solution was added 2 μl of an SDS sampling buffer (125 mM Tris-hydrochloric acid buffer solution, pH 6.8, 120 mM 2-mercaptoethanol, 2% SDS solution, 0.025% bromophenol blue, and 20% glycerol) and the resulting solution was heated at 95°C for 3 minutes and then subjected to SDS-polyacrylamide gel electrophoresis. The molecular weight of the translation product was determined by carrying out the autoradiography.

(7) Northern Blot Hybridization

The northern blot hybridization was carried out in order to examine the expression pattern in the human tissues. Membranes on which poly(A)$^+$ RNAs isolated from each of the human tissues are blotted are purchased from Clontech Inc. cDNA fragments which were excised from the objective clones with appropriate restriction enzymes were subjected to separation by agarose gel electrophoresis followed by labeling with [^{32}P] dCPT (Amersham Corporation) using the Random Primer Labeling Kit (Takara Shuzo Co., Ltd.). Hybridization was carried out using a solution attached to the blotted membrane in accordance to the protocol.

(8) Expression in COS7

Escherichia coli having an expression vector of the protein of the invention was infected with helper phage M13KO7, and single stranded phage was obtained by the above method. Using the thus obtained phage, the expression vector was introduced into simian kidney-originated culture cells COS7 according to the above method. Cultivation was carried out at 37°C in the presence of 5 % CO_2 for 2 hours and then in a medium containing [^{35}S]cysteine for 1 hour. The cells

were collected, dissolved and subjected to SDS-PAGE, whereby a band corresponding to a protein as the expression product, which was not present in the COS cells, was revealed.

(9) Clone Examples

<HP00442> (Sequence Number 1, 26, 51)

Determination of the whole base sequence for the cDNA insert of clone HP00442 obtained from the human fibrosarcoma cell line HT-1080 cDNA libraries revealed the structure consisting of a 5'-non-translation region of 81 bp, an ORF of 618 bp, and a 3'-non-translation region of 287 bp. The ORF codes for a protein consisting of 205 amino acid residues with 5 transmembrane domains. Figure 2 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. The result of the in vitro translation did not reveal the formation of distinct bands for the translation products and revealed the formation of smeary bands at the high-molecular-weight position.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was analogous to the proteolipid protein PPA1 of the baker's yeast proton ATPase (SWISS-PROT Accession No. P23968). Table 2 indicates the comparison of the amino acid sequences between the human protein of the present invention (HP) and the proteolipid protein PPA1 of the baker's yeast proton ATPase (PL). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and . represents an amino acid residue analogous to that in the protein of the present invention. The both proteins possessed a homology of 56.8% in the entire region

except for the N-terminal.

Table 2

```
HP           MTGLALLYSGVFVAFWACALAVGVCYTIF-DLGFRFDVAWFLTETSPFMWS

                                           *..* . *  .. . **  ***.**.

PL    MNKESKDDDMSLGKFSFSHFLYYLVLIVVIVYGLYKLFTGHGSDINFGKFLLRTSPYMWA

HP    NLGIGLAISLSVVGAAWGIYITGSSIIGGGVKAPRIKTKNLVSIIFCEAVAIYGIIMAIV

      ****.* ..**********.*****.**.**.****.****.******.*****.*.***

PL    NLGIALCVGLSVVGAAWGIFITGSSMIGAGVRAPRITTKNLISIIFCEVVAIYGLIIAIV

HP    ISNMAEPFSATDPKAIGHRNYHAGYSMFGAGLTVGLSNLFCGVCVGIVGSGAALADAQNP

      .*..     **. .  ...* ..***.* **.*** ***.**. ***.*..**..**...

PL    FSSKL--TVATAENMYSKSNLYTGYSLFWAGITVGASNLICGIAVGITGATAAISDAADS

HP    SLFVKILIVEIFGSAIGLFGVIVAILQTSRVKMGD

      .******..***** .**.*.**..* ...

PL    ALFVKILVIEIFGSILGLLGLIVGLLMAGKASEFQ
```

Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more and also containing the initiation codon (for example, Accession No. H87379), but the present protein can not be predicted from this sequence.

The proteolipid protein PPA1 of the baker's yeast proton ATPase is a membrane protein essential to the growth

of cells [Apperson, M. et al., Biochem. Biophys. Res. Commun. 168: 574-579 (1990)]. Accordingly, the protein of present invention, which is homologous to said protein, is considered to be essential to the growth of human cells and can be utilized for the diagnosis and the treatment of diseases caused by the abnormality of the present protein.

<HP00804> (Sequence Number 2, 27, 52)

Determination of the whole base sequence for the cDNA insert of clone HP00804 obtained from the human leukocyte cell cDNA libraries revealed the structure consisting of a 5'-non-translation region of 132 bp, an ORF of 1116 bp, and a 3'-non-translation region of 576 bp. The ORF codes for a protein consisting of 371 amino acid residues with 7 transmembrane domains. Figure 3 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle. The result of the in vitro translation did not reveal the formation of distinct bands for the translation products.

Examination of the expression pattern in the tissues by the northern blot hybridization using the cDNA fragment of the present invention revealed that the expression occurred in all tissues examined as shown in Figure 4. Therefore, the protein of the present invention is considered to be a housekeeping protein.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was analogous to the rat NMDA receptor - glutamate-binding subunit (GenBank Accession No. S61973). Table 3 indicates the comparison of the amino acid sequences

between the human protein of the present invention (HP) and the rat NMDA receptor - glutamate-binding subunit (RN). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and represents an amino acid residue analogous to that in the protein of the present invention. This subunit consists of 516 amino acid residues and a region from glutamine at position 68 to arginine at position 342 possessed a 92.6 % homology with the C-terminal 270 amino acid residues in the protein of the present invention. However, any homology was not observed in the N-terminal region. Hereupon, a characteristic repeated sequence that is rich with proline, tyrosine, and glycine was observed in the N-terminal region of the protein of the present invention.

Table 3

```
HP  MSHEKSFLVSGDNYPPPNPGYPGGPQPPMPPYAQPPYPGAPYPQPPFQPSPYGQPGYPHG

RN                                MKRVSWSLGTAILPQTLAILWGHKPLCLPMFSLPTLG
HP  PSPYPQGGYPQGPYPQGGYPQGPYPQEGYPQGPYPQGGYPQGPYPQSPFPPNPYGQPQVF
                                             **.***************. *
RN  PHTHRPLSSPLPMVNQGIPMVPVPITRWLPLKDLLKEATHQGHYPQSPFPPNPYGQPPPF
HP  PGQDPDSPQHGNYQEEGPPSYYDNQDFPATNWDDKSIRQAFIRKVFLVLTLQLSVTLSTV
      ***.**********************..** ***************************
RN  --QDPGSPQHGNYQEEGPPSYYDNQDFPSVNW-DKSIRQAFIRKVFLVLTLQLSVTLSTV
HP  SVFTFVAEVKGFVRENVWTYYVSYAVFFISLIVLSCCGDFRRKHPWNLVALSVLTASLSY
```

```
   ..****.*******.**********.***************.**********.** ****
RN AIFTFVGEVKGFVRANVWTYYVSYAIFFISLIVLSCCGDFRKKHPWNLVALSILTISLSY
HP MVGMIASFYNTEAVIMAVGITTAVCFTVVIFSMQTRYDFTSCMGVLLVSMVVLFIFAILC
   ************************************************.**********
RN MVGMIASFYNTEAVIMAVGITTAVCFTVVIFSMQTRYDFTSCMGVLLVSVVVLFIFAILC
HP IFIRNRILEIVYASLGALLFTCFLAVDTQLLLGNKQLSLSPEEYVFAALNLYTDIINIFL
   ************************************************************
RN IFIRNRILEIVYASLGALLFTCFLAVDTQLLLGNKQLSLSPEEYVFAALNLYTDIINIFL
HP YILTIIGRAKE
   ********..
RN YILTIIGRSQGIGQAPAQVAWWAQTHAPAMTLPSVLPPLWFPAMAWSRGSPSRPRVCTLQ
```

Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. W25936), but any of them was shorter than the present cDNA and did not contain the initiation codon.

The rat NMDA receptor - glutamate-binding subunit has been found as one of the subunits of the NMDA receptor complex which exists specifically in the brain [Kumar. K. N. et al., Nature 354: 70-73 (1991)]. Despite a high homology with the protein of the present invention, the subunit shows different expression patterns in the N-terminal sequence and the tissues, whereby both molecules are considered to possess different functions. Since the protein of the present invention possesses 7 transmembrane

domains which are characteristic to channels and transporters, this protein is considered to play a role as a channel and a transporter. Because the protein of the present invention is a housekeeping protein essential to the cells, the present protein can be utilized for the diagnosis and the treatment of diseases caused by the abnormality of this protein.

<HP01098> (Sequence Number 3, 28, 53)

Determination of the whole base sequence for the cDNA insert of clone HP01098 obtained from the human stomach cancer cDNA libraries revealed the structure consisting of a 5'-non-translation region of 61 bp, an ORF of 540 bp, and a 3'-non-translation region of 475 bp. The ORF codes for a protein consisting of 179 amino acid residues with one transmembrane domain. Figure 5 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. The in vitro translation resulted in the formation of a translation product of 20 kDa that was almost consistent with the molecular weight of 20,625 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was completely identical with a 18-kDa subunit of the canine microsomal signal peptidase (SWISS-PROT Accession No. P21378). Therefore, it was verified that the cDNA of the present invention codes for the human homologue of the 18-kDa subunit of the microsomal signal peptidase.

The search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs

possessing the homology of 90% or more (for example, Accession No. T60549), but many sequences were not distinct and the same ORF as that in the present cDNA was not identified.

The 18-kDa subunit of the canine microsomal signal peptidase has been found as one of subunits of the signal peptidase complex that exist in the microsome [Schelness, G. S. & Blobel, G., J. Biol. Chem. 265: 9512-9519 (1990)]. The signal peptidase is an enzyme that cleaves the signal sequence upon secretion of a secretory protein at the endoplasmic reticulum. Therefore, the cDNA of the present invention can be utilized for the production of the present protein as well as for the diagnosis and the treatment of diseases caused by the abnormality of the present protein.

<HP01148> (Sequence Number 4, 29, 54)

Determination of the whole base sequence for the cDNA insert of clone HP01148 obtained from the human liver cDNA libraries revealed the structure consisting of a 5'-non-translation region of 101 bp, an ORF of 1044 bp, and a 3'-non-translation region of 446 bp. The ORF codes for a protein consisting of 347 amino acid residues with one transmembrane domain at the N-terminal. Figure 6 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. It was indicated that the present protein remained in the membrane from the observation that the urokinase secretion was not identified, upon transduction into the COS7 cells of an expression vector in which a HindIII-PvuII fragment containing a cDNA fragment encoding the N-terminal 178

amino acid residues in the present protein was inserted at the HindIII-PmaCI site of pSSD3. Therefore, the present protein is considered to be a type-II membrane protein. The in vitro translation resulted in the formation of a translation product of 41 kDa that was almost consistent with the molecular weight of 38,101 predicted from the ORF.

Examination of the expression pattern in the tissues by the northern blot hybridization using the cDNA fragment of the present invention revealed that a strong expression occurred in the spleen, as shown in Figure 7. It was also indicated that a slight expression occurred in the liver.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was analogous to the bovine WC1 antigen (SWISS-PROT Accession No. P30205). Table 4 indicates the comparison of the amino acid sequences between the human protein of the present invention (HP) and the bovine WC1 antigen (WC). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and . represents an amino acid residue analogous to that in the protein of the present invention. The both proteins possessed a homology of 38%.

Table 4

```
HP          MALLFSLILAICTRPGFLASPSGVRLVGGLHRCEGRVEVEQKGQWGTVCDDGW
                               . .... .***.*  .*.****. ..* ***.***.*
WC   VLPQCNDFLSQPAGSAASEESSPYCSDSRQLRLVDGGGPCGGRVEILDQGSWGTICDDDW
```

```
HP   DIKDVAVLCRELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEE--V

     *..*. *.**.****.* .....  .   .. .  . .....***.*. . .*   .

WC   DLDDARVVCRQLGCGEALNATGSAHF---GAGSGPIWLDDLNCTGKESHVWRCPSRGWGR

HP   YDCSHEEDAGASCENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQTGWSLRA

     .**.*.****. *  .*  *      ..*....  .* *..** ... * .**..  .  .

WC   HDCRHKEDAGVIC--SE--F----LALRMVSEDQQCAGWLEVFYNGTWGSVCRSPMEDIT

HP   AKVVCRQLGCGRAVLTQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHD

     ..*.******* .   ... . .. *..* *.. . *. ....* .******  ..*...

WC   VSVICRQLGCGDSGSLNTSVGLRE-GSRPRWVDLIQCRKMDTSLWQCPSGPWKYSSCSPK

HP   EDTWVECE--------------DPFDLRLVGGDNLCSGRLEVLHKGVWGSVCDDNWGEKE

     *.....**              *. .*** ***. ****.** *.* **.****.*.  *

WC   EEAYISCEGRRPKSCPTAAACTDREKLRLRGGDSECSGRVEVWHNGSWGTVCDDSWSLAE

HP   DQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWLDNVRCSGEEQSLEQCQHRFWGFHDCTH

     ..***.*****..*. . * .  .*** *.****.*.*.* * ** .*    **  **.*

WC   AEVVCQQLGCGQALE-AVR-SAAFGPGNGSIWLDEVQCGGRESSLWDCVAEPWGQSDCKH

HP   QEDVAVICSG

     .**..* ***

WC   EEDAGVRCSGVRTTLPTTTAGTRTTSNSLPGIFSLPGVLCLILGSLLFLVLVILVTQLLR
```

Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. H91200), but it can not be assessed whether these ESTs with partial sequences code for the same protein as the protein of the present invention.

The bovine WC1 antigen has been found as a membrane

antigen which is expressed specifically in $\gamma\delta$ T cells [Wijngaard, P. L. J. et al., J. Immunol. 149: 3273-3277 (1992)]. The region showing an analogy is called the scavenger receptor cysteine-rich domain (SRCR) which also exists as a repeated sequence in macrophage scavenger receptors [Matsumoto, A. et al., Proc. Natl. Acad. Sci. USA 87: 9133-9137 (1990)], T cell differentiation antigen CD6 [Aruffo, A. et al., J. Exp. Med. 174: 949-952 (1991)], and so on. Since the present protein is expressed specifically in the spleen, This protein is considered to be deeply associated with the functions of the spleen and also to function as a receptor in the same manner as other SRCR family members.

<HP01293> (Sequence Number 5, 30, 55)

Determination of the whole base sequence for the cDNA insert of clone HP01293 obtained from the human liver cDNA libraries revealed the structure consisting of a 5'-non-translation region of 89 bp, an ORF of 1665 bp, and a 3'-non-translation region of 134 bp. The ORF codes for a protein consisting of 554 amino acid residues with 12 transmembrane domains. Figure 8 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. The in vitro translation did not reveal the formation of distinct bands and revealed the formation of smeary bands at the high-molecular-weight position.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was analogous to the rat cation transporter

(GenBank Accession No. X78855). Table 5 indicates the comparison of the amino acid sequences between the human protein of the present invention (HP) and the mouse interstitial cell protein (MM). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and . represents an amino acid residue analogous to that in the protein of the present invention. The both proteins possessed a homology of 78.1% among the entire regions.

Table 5

```
HP  MPTVDDILEQVGESGWFQKQAFLILCLLSAAFAPICVGIVFLGFTPDHHCQSPGVAELSQ
    ******.****** *********.***.**..***.**********.*.**.********
RN  MPTVDDVLEQVGEFGWFQKQAFLLLCLISASLAPIYVGIVFLGFTPGHYCQNPGVAELSQ
HP  RCGWSPAEELNYTVPGLGPAGEA-FLGQCRRYEVDWNQSALSCVDPLASLATNRSHLPLG
    *****.**************..** **.**.**********.*.*****.**..***.****
RN  RCGWSQAEELNYTVPGLGPSDEASFLSQCMRYEVDWNQSTLDCVDPLSSLVANRSQLPLG
HP  PCQDGWVYDTPGSSIVTEFNLVCADSWKLDLFQSCLNAGFFFGSLGVGYFADRFGRKLCL
    **..*******************.*.**.******.* ***.*** ***.**********
RN  PCEHGWVYDTPGSSIVTEFNLVCGDAWKVDLFQSCVNLGFFLGSLVVGYIADRFGRKLCL
HP  LGTVLVNAVSGVLMAFSPNYMSMLLFRLLQGLVSKGNWMAGYTLITEFVGSGSRRTVAIM
    * *.**..***** * .*.* **********.****.*..************ ***.**.
RN  LVTTLVTSVSGVLTAVAPDYTSMLLFRLLQGMVSKGSWVSGYTLITEFVGSGYRRTTAIL
HP  YQMAFTVGLVALTGLAYALPHWRWLQLAVSLPTFLFLLYYWCVPESPRWLLSQKRNTEAI
    **********.*.*.***.*.******************** *************.* *.
```

```
RN   YQMAFTVGLVGLAGVAYAIPDWRWLQLAVSLPTFLFLLYYWFVPESPRWLLSQKRTTRAV

HP   KIMDHIAQKNGKLPPADLKMLSLEEDVTEKLSPSFADLFRTPRLRKRTFILMYLWFTDSV
     .**..*******.********.****..** ***********.***.* *******. .*
RN   RIMEQIAQKNGKVPPADLKMLCLEEDASEKRSPSFADLFRTPNLRKHTVILMYLWFSCAV

HP   LYQGLILHMGATSGNLYLDFLYSALVEIPGAFIALITIDRVGRIYPMAVSNLLAGAACLV
     ******.*.***..******.**.***.*.*** *.****.*****.*.***..*****.
RN   LYQGLIMHVGATGANLYLDFFYSSLVEFPAAFIILVTIDRIGRIYPIAASNLVTGAACLL

HP   MIFISPDLHWLNIIIMCVGRMGITIAIQMICLVNAELYPTFVRNLGVMVCSSLCDIGGII
     ****...*****... *.**** **..**.***********.****.****.***.***.
RN   MIFIPHELHWLNVTLACLGRMGATIVLQMVCLVNAELYPTFIRNLGMMVCSALCDLGGIF

HP   TPFIVFRLREVWQALPLILFAVLGLLAAGVTLLLPETKGVALPETMKDAENLG-RKAKPK
     ***.****.***********.**** *...****************...***** **.*.*
RN   TPFMVFRLMEVWQALPLILFGVLGLTAGAMTLLLPETKGVALPETIEEAENLGRRKSKAK

HP   ENTIYLKVQTSEPSGT
     ******.***...*.*
RN   ENTIYLQVQTGKSSST
```

Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there did not exist any human gene and human EST possessing the homology of 90% or more.

The rat cation transporter has been found as a membrane protein that relates to the drug excretion in the kidney [Grundemann, D. et al., Nature 372: 549-552 (1994)]. Accordingly, the protein of the present invention which is homologous to this transporter is considered to possess a

similar function and can be utilized for the diagnosis and the treatment of diseases caused by the abnormality of this protein. In addition, since the present protein is considered to relate to the drug excretion, the cells in which this protein is expressed can be utilized as a tool for the drug design of these drugs. Furthermore, since the present protein is expressed principally in the liver and the kidney, a molecule that is prepared so as to possess an affinity to this protein is applicable for the drug delivery system into these tissues.

<HP10013> (Sequence Number 6, 31, 56)

Determination of the whole base sequence for the cDNA insert of clone HP10013 obtained from the human epidermoid carcinoma cell line KB cDNA libraries revealed the structure consisting of a 5'-non-translation region of 96 bp, an ORF of 1053 bp, and a 3'-non-translation region of 884 bp. The ORF codes for a protein consisting of 350 amino acid residues with a signal sequence at the N-terminal and one internal transmembrane domain. Figure 9 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. It was indicated that the present protein functioned as a signal sequence at the N-terminal from the observation that the urokinase activity was detected in the culture medium, upon transduction into the COS7 cells of an expression vector in which a HindIII-Eco065I fragment (treated with the mung-bean nuclease) containing a cDNA fragment encoding the N-terminal 65 amino acid residues in the present protein was inserted at the HindIII-EcoRV site of pSSD3. Therefore, the

present protein is considered to be a type-I membrane protein. The in vitro translation resulted in the formation of a translation product of 39 kDa that was almost consistent with the molecular weight of 39,008 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was not analogous to any of known proteins. Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. H07998), but any of them was shorter than the present cDNA and did not contain the initiation codon.

<HP10034> (Sequence Number 7, 32, 57)

Determination of the whole base sequence for the cDNA insert of clone HP10034 obtained from the human fibrosarcoma cell line HT-1080 cDNA libraries revealed the structure consisting of a 5'-non-translation region of 175 bp, an ORF of 630 bp, and a 3'-non-translation region of 106 bp. The ORF codes for a protein consisting of 209 amino acid residues with 4 transmembrane domains. Figure 10 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. The in vitro translation resulted in the formation of a translation product of 21 kDa that was almost consistent with the molecular weight of 22,432 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was analogous to the human tumor-associated antigen

L6 (SWISS-PROT Accession No. P30408). Table 6 indicates the comparison of the amino acid sequences between the human protein of the present invention (HP) and the human tumor-associated antigen L6 (L6). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and . represents an amino acid residue analogous to that in the protein of the present invention. The both proteins possessed a homology of 31.8%.

Table 6

```
HP  MVSSPCTQASSRTCSRILGLSLGTAALFAAGANVALLLPNWDVTYLLRGLLGRHAMLGTG
                 *.* .* ** . **.  .**. * .** ...*    .*.* . . .*
L6          MCYGKCARCIGHSLVGLALLCIAANILLYFPNGETKYASENHLSRFVWFFSG
HP  LWGGGLMVLTAA-ILISL-MGWRYGCFS--KSGLCRSVLTALLSGGLALLGALICFVTSG
    . ****..* .* ..*.* .   .** .  ..*   ..*...*.. ... *.  * ....
L6  IVGGGLIMLLPAFVFIGLEQDDCCGCCGHENCGKRCAMLSSVLAALIGIAGSGYCVIVAA
HP  VALKDGPFCMFDVSSFNQTQAWKYGYPFKDLHSRNYLYDRSLWNSVCLEPSAAVVWHVSL
    ..* .**.*. *        .*.*... ..    .** * * *.. * **.  * *.***
L6  LGLAEGPLCL-D-----SLGQWNYTFASTE---GQYLLDTSTWSE-CTEPKHIVEWNVSL
HP  FSALLCISLLQLLLVVVHVINSLLGLFCSLCEK
    ** ** .. ....* ...***..**..*..*
L6  FSILLALGGIEFILCLIQVINGVLGGICGFCCSHQQQYDC
```

Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there did not exist any human gene and human EST possessing the homology of 90% or more.

The human tumor-associated antigen L6 is a member of the membrane antigen TM4 super-family proteins that are expressed abundantly on the cell surface of human tumors [Marken, J. S. et al., Proc. Natl. Acad. Sci. USA 89: 3503-3507 (1992)]. Since these membrane antigens are expressed specifically in specific cells and in cancer cells, an antibody that is prepared so as to bind to this antigen is applicable for a variety of diagnoses and as a carrier for the drug delivery. Furthermore, cells in which such a membrane antigen is expressed by transduction of the membrane antigen gene are applicable to the detection of the corresponding ligand.

<HP10050> (Sequence Number 8, 33, 58)

Determination of the whole base sequence for the cDNA insert of clone HP10050 obtained from the human fibrosarcoma cell line HT-1080 cDNA libraries revealed the structure consisting of a 5'-non-translation region of 9 bp, an ORF of 492 bp, and a 3'-non-translation region of 100 bp. The ORF codes for a protein consisting of 163 amino acid residues with one transmembrane domain. Figure 11 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. The in vitro translation resulted in the formation of a translation product of 23 kDa that was almost consistent with the molecular weight of 18,364 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was not analogous to any of known proteins. Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. H03117), but many sequences were not distinct and the same ORF as that in the present cDNA was not identified.

<HP10071> (Sequence Number 9, 34, 59)

Determination of the whole base sequence for the cDNA insert of clone HP10071 obtained from the human stomach cancer cDNA libraries revealed the structure consisting of a 5'-non-translation region of 46 bp, an ORF of 279 bp, and a 3'-non-translation region of 69 bp. The ORF codes for a protein consisting of 92 amino acid residues with 2 transmembrane domains. Figure 12 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. The in vitro translation resulted in the formation of a translation product of 12 kDa that was almost consistent with the molecular weight of 10,094 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was not analogous to any of known proteins. Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. R097442), but many sequences were not

distinct and the same ORF as that in the present cDNA was not identified.

<HP10076> (Sequence Number 10, 35, 60)

Determination of the whole base sequence for the cDNA insert of clone HP10076 obtained from the human lymphoma cell line U937 cDNA libraries revealed the structure consisting of a 5'-non-translation region of 81 bp, an ORF of 519 bp, and a 3'-non-translation region of 132 bp. The ORF codes for a protein consisting of 172 amino acid residues with 2 transmembrane domains. Figure 13 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. It was indicated that the present protein remained in the membrane from the observation that the urokinase secretion was not identified upon transduction into the COS7 cells of an expression vector in which a HindIII-Eco0651 (treated with mung-bean nuclease) fragment containing a cDNA fragment encoding the N-terminal 167 amino acid residues in the present protein was inserted at the HindIII-EcoRV site of pSSD3. The in vitro translation resulted in the formation of a translation product of 24 kDa that was almost consistent with the molecular weight of 18,450 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was analogous to the baker's yeast hypothetical membrane protein of 23.1 kDa (SWISS-PROT Accession No. P34222). Table 7 indicates the comparison of the amino acid sequences between the human protein of the present

invention (HP) and the baker's yeast hypothetical membrane protein of 23.1 kDa (SC). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and . represents an amino acid residue analogous to that in the protein of the present invention. The both proteins possessed a homology of 47.5% in the C-terminal region of 139 amino acid residues.

Table 7

```
HP                            MEYLAHPSTLGLAVGVACGMCLGWS

SC  MITSFLMEKMTVSSNYTIALWATFTAISFAVGYQLGTSNASSTKKSSATLLRSKEMKEGK
HP  LRVCFGMLPKSKTSKTHTDTESEASILGD-SGEYKMILVVRNDLKMGKGKVAAQCSHAAV
                 ...*.. *.. *.* .** .* **.*.** *.***.****.***.
SC  LHNDTDEEESESEDESDEDEDIESTSLNDIPGEVRMALVIRQDLGMTKGKIAAQCCHAAL
HP  SAYKQI------QRRNPEMLKQWEYCGQPKVVVKAPDEETLIALLAHAKMLGLTVSLIQD
    * ...*      .. ** * ..*   **.*...* **. *. .* *.*  **.....*.*
SC  SCFRHIATNPARASYNPIMTQRWLNAGQAKITLKCPDKFTMDELYAKAISLGVNAAVIHD
HP  AGRTQIAPGSQTVLGIGPGPADLIDKVTGHLKLY
    *******.**.****.**.* ...*..**.****
SC  AGRTQIAAGSATVLGLGPAPKAVLDQITGDLKLY
```

Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed

some ESTs possessing the homology of 90% or more (for example, Accession No. T74847), but many sequences were not distinct and the same ORF as that in the present cDNA was not identified.

<HP10085> (Sequence Number 11, 36, 61)

Determination of the whole base sequence for the cDNA insert of clone HP10085 obtained from the human lymphoma cell line U937 cDNA libraries revealed the structure consisting of a 5′-non-translation region of 150 bp, an ORF of 450 bp, and a 3′-non-translation region of 97 bp. The ORF codes for a protein consisting of 149 amino acid residues with one transmembrane domain at the N-terminal. Figure 14 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. It was indicated that the present protein remained in the membrane from the observation that the urokinase secretion was not identified upon transduction into the COS7 cells of an expression vector in which a HindIII-EcoRI fragment (after the Klenow treatment) containing a cDNA fragment encoding the N-terminal 57 amino acid residues in the present protein was inserted at the HindIII-EcoRV site of pSSD3. Therefore, the present protein is considered to be a type-II membrane protein. The in vitro translation resulted in the formation of a translation product of 20 kDa that was almost consistent with the molecular weight of 17,307 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was analogous to the human early activation antigen

CD69 (SWISS-PROT Accession No. Q07108). Table 8 indicates the comparison of the amino acid sequences between the human protein of the present invention (HP) and the human early activation antigen CD69 (CD). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and . represents an amino acid residue analogous to that in the protein of the present invention. The both proteins possessed a homology of 36.6% in the C-terminal region of 112 amino acid residues.

Table 8

```
HP                                            MMTKHKKCFI

CD  MSSENCFVAENSSLHPESGQENDATSPHFSTRHEGSFQVPVLCAVMNVVFITILIIALIA
HP  IVGVLITTNIITLIVKLTRDSQSLCPYDWIGFQNKCYYFSKEEGDWNSSKYNCSTQHADL
                          * *. **.*.*.***..*. . .*.*.. .**.. *.*
CD  LSVGQYNCPGQYTFSMPSDSHVSSCSEDWVGYQRKCYFISTVKRSWTSAQNACSEHGATL
HP  TIIDNIEEMNFLRRYKCSSDHWIGLKMAKNRTGQWVDGATFTKSFGMRGSEGCAYLSDDG
    ..**. ..****.**  ...**.***.. ... .* .* .*.. *.. **. *..*....
CD  AVIDSEKDMNFLKRYAGREEHWVGLKKEPGHPWKWSNGKEFNNWFNVTGSDKCVFLKNTE
HP  AATARCYTERKWICRKRIH
    ... * .. ***.*
CD  VSSMECEKNLYWICNKPYK
```

Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. H11808), but many sequences are not distinct and the same ORF as that in the present cDNA was not identified.

The human early activation antigen CD69 is a glycoprotein that appears on the surface of activated lymphocytes and a member of the C-type lectin super-family [Hamann, J. et al., J. Immunol. 150: 4920-4927 (1993)]. Since these membrane antigens are expressed specifically in some specific cells, an antibody that is prepared so as to bind to this antigen is applicable for a variety of diagnoses and as a carrier for the drug delivery. Furthermore, cells in which such a membrane antigen is expressed by transduction of the membrane antigen gene are applicable to the detection of the corresponding ligand.

<HP10122> (Sequence Number 12, 37, 62)

Determination of the whole base sequence for the cDNA insert of clone HP10122 obtained from the human stomach cancer cDNA libraries revealed the structure consisting of a 5'-non-translation region of 138 bp, an ORF of 567 bp, and a 3'-non-translation region of 481 bp. The ORF codes for a protein consisting of 188 amino acid residues with 2 transmembrane domains. Figure 15 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. The in vitro translation resulted in the formation of a translation product of 22 kDa that was almost consistent with the

molecular weight of 21,175 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was not analogous to any of known proteins. Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. T80360), but many sequences were not distinct and the same ORF as that in the present cDNA was not identified.

<HP10136> (Sequence Number 13, 38, 63)

Determination of the whole base sequence for the cDNA insert of clone HP10136 obtained from the human lymphoma cell line U937 cDNA libraries revealed the structure consisting of a 5'-non-translation region of 81 bp, an ORF of 648 bp, and a 3'-non-translation region of 680 bp. The ORF codes for a protein consisting of 215 amino acid residues with one transmembrane domain at the C-terminal. Figure 16 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. The in vitro translation resulted in the formation of a translation product of 28 kDa that was almost consistent with the molecular weight of 24,740 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was analogous to the baker's yeast protein transport protein SLY2 (SWISS-PROT Accession No. P22214). Table 9 indicates the comparison of the amino acid

sequences between the human protein of the present invention (HP) and the baker's yeast protein transport protein SLY2 (SC). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and . represents an amino acid residue analogous to that in the protein of the present invention. The both proteins possessed a homology of 36.1% in the entire regions.

Table 9

```
HP   MVLLTMIARVADGLPLAASMQEDEQSGRDLQQYQSQAKQLFRKLNEQSPTRCTLEAGAMT
     *.  *.* *  ***** .*........  * . . ..* . ..*. **.*  ***.*...
SC   MIKSTLIYRE-DGLPLCTSVDNENDPS--LFEQKQKVKIVVSRLTPQSATEATLESGSFE

HP   FHYIIEQGVCYLVLCEAAFPKKLAFAYLEDLHSEFDEQHGKKVPTVS-RPYSFIEFDTFI
     .**. .  *.*.*.**...*..***.**.*.  **..  ... *. . *** *..**.*.
SC   IHYLKKSMVYYFVICESGYPRNLAFSYLNDIAQEFEHSFANEYPKPTVRPYQFVNFDNFL

HP   QKTKKLYIDSRARRNLGSINTELQDVQRIMVANIEEVLQRGEALSALDSKANNLSSLSKK
     *.*** * *.... **. .* ** .*..**  ***..* **..*. .......*.. **.
SC   QMTKKSYSDKKVQDNLDQLNQELVGVKQIMSKNIEDLLYRGDSLDKMSDMSSSLKETSKR

HP   YRQDAKYLNMRSTYAKLAAVAVFFIMLIVYVRFWWL
     **..*. .*.    .. *.. *.  ...*.. ***.
SC   YRKSAQKINFDLLISQYAPI-VIVAFFFVFL-FWWIFLK
```

Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed

some ESTs possessing the homology of 90% or more (for example, Accession No. R80136), but they were shorter than the present cDNA and any molecule containing the initiation codon was not identified.

The baker's yeast protein transport protein SLY2 has been known to be essential for endoplasmic reticulum-to-Golgi protein transport and to be also associated with the control of the cell cycle [Dascher, C. et al., Mol. Cell. Biol. 11: 872-885 (1991)]. Therefore, the cDNA of the present invention can be utilized for the production of the present protein as well as for the diagnosis and the treatment of diseases caused by the abnormality of the present protein.

<HP10175> (Sequence Number 14, 39, 64)

Determination of the whole base sequence for the cDNA insert of clone HP10175 obtained from the human stomach cancer cDNA libraries revealed the structure consisting of a 5'-non-translation region of 173 bp, an ORF of 339 bp, and a 3'-non-translation region of 462 bp. The ORF codes for a protein consisting of 112 amino acid residues with 4 transmembrane domains. Figure 17 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. The result of the in vitro translation resulted in the formation of a translation product of 13 kDa that was almost consistent with the molecular weight of 11,564 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was not analogous to any known proteins.

Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. W52852), but many sequences were not distinct and the same ORF as that in the present cDNA was not identified.

<HP10179> (Sequence Number 15, 40, 65)

Determination of the whole base sequence for the cDNA insert of clone HP10179 obtained from the human epidermoid carcinoma cell line KB cDNA libraries revealed the structure consisting of a 5'-non-translation region of 121 bp, an ORF of 345 bp, and a 3'-non-translation region of 459 bp. The ORF codes for a protein consisting of 114 amino acid residues with 4 transmembrane domains. Figure 18 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. The in vitro translation resulted in the formation of a translation product of 14 kDa that was almost consistent with the molecular weight of 12,078 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was not analogous to any known proteins. However, this protein was analogous to the protein encoded by the cDNA clone Hp 10175 of the present invention. Table 10 indicates the comparison of the amino acid sequences between the protein encoded by HP 10179 and the protein encoded by HP 10175. - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and . represents an amino acid residue

analogous to that in the protein of the present invention. The both proteins possessed a homology of 80.8% in the entire regions.

Table 10

```
179 MEKPLFPLVPLHWFGFGYTALVVSGGIVGYVKTGSVPSLAAGLLFGSLAGLGAYQLYQDP
          ..**********.***.****.****.*********************** ***
175  MQDTGSVVPLHWFGFGYAALVASGGIIGYVKAGSVPSLAAGLLFGSLAGLGAYQLSQDP

179 RNVWGFLAATSVTFVGVMGMRSYYYGKFMPVGLIAGASLLMAAKVGVRMLMTSD
    **** ** *** *..*.**** *. *****.**********.*****.*.
175 RNVWVFL-ATSGTLAGIMGMRFYHSGKFMPAGLIAGASLLMVAKVGVSMFNRPH
```

Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. N55991), but many sequences were not distinct and the same ORF as that in the present cDNA was not identified.

<HP10196> (Sequence Number 16, 41, 66)

Determination of the whole base sequence for the cDNA insert of clone HP10196 obtained from the human fibrosarcoma cell line HT-1080 cDNA libraries revealed the structure consisting of a 5'-non-translation region of 9 bp, an ORF of 984 bp, and a 3'-non-translation region of 122 bp. The ORF codes for a protein consisting of 327 amino acid residues with one transmembrane domain at the N-

terminal. Figure 19 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. It was indicated that the present protein remained in the membrane from the observation that the urokinase secretion was not identified upon transduction into the COS7 cells of an expression vector in which a HindIII-BglII fragment (after the Klenow treatment) containing a cDNA fragment encoding the N-terminal 162 amino acid residues in the present protein was inserted at the HindIII-EcoRV site of pSSD3. Therefore, the present protein is considered to be a type-II membrane protein. The in vitro translation resulted in the formation of a translation product of 37 kDa that was almost consistent with the molecular weight of 36,163 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was not analogous to any known proteins. Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. T17026), but they were shorter than the present cDNA and any molecule containing the initiation codon was not identified.

<HP10235> (Sequence Number 17, 42, 67)

Determination of the whole base sequence for the cDNA insert of clone HP10235 obtained from the human fibrosarcoma cell line HT-1080 cDNA libraries revealed the structure consisting of a 5'-non-translation region of 5

bp, an ORF of 1122 bp, and a 3'-non-translation region of 594 bp. The ORF codes for a protein consisting of 373 amino acid residues with 11 transmembrane domains. Figure 20 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. The in vitro translation did not reveal the formation of distinct bands and revealed the formation of smeary bands at the high-molecular-weight position.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was analogous to the human nucleolar protein HNP36 (EMBL Accession No. X86681). Table 11 indicates the comparison of the amino acid sequences between the human protein of the present invention (HP) and the human nucleolar protein HNP36 (NP). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and . represents an amino acid residue analogous to that in the protein of the present invention. The both proteins possessed a homology of 45.3% in the entire regions.

Table 11

```
HP  MTLCAMLPLLLFTYLNSFLHQRIPQSVRILGSLVAILLVFLITAILVKVQLDALPFFVIT

HP  MIKIVLINSFGAILQGSLFGLAGLLPASYTAPIMSGQGLAGFFASVAMICAIASGSELSE
    *  ..  .****.*.*******  *  .*..*..  ..*******.**..**.  ..***  .  ..
NP  MASVCFINSFSAVLQGSLFGQLGTMPSTYSTLFLSGQGLAGIFAALAMLLSMASGVDAET
```

```
HP  SAFGYFITACAVIILTIICYLGLPRLEFYRYYQQLKLEGPGEQE--TKLDLISKGEE---
    **.*****... *...*.***.**.*.* *** . * . . .**  ** .*. ..*.
NP  SALGYFITPYVGILMSIVCYLSLPHLKFARYYLANKSSQAQAQELETKAELLQSDENGIP

HP  --PRAGKEESGVSV---SNSQPTNESHSIK----AILKNISVLAFSVCFIFTITIGMFPA
      *.    . ....   ..*.*..  .. *    .....* . *... ..**.*...***
NP  SSPQKVALTLDLDLEKEPESEPDEPQKPGKPSVFTVFQKIWLTALCLVLVFTVTLSVFPA

HP  VTVEVKSSIAGSSTWERYFIPVSCFLTFNIFDWLGRSLTAVFMWPGKDSRWLPSLVLARL
    .*. *.** .....*...* *..*** ***.********. *.**..*** ** **  *.
NP  ITAMVTSS-TSPGKWSQFFNPICCFLLFNIMDWLGRSLTSYFLWPDEDSRLLPLLVCLRF

HP  VFVPLLLLCNIKPRRYLTVVFEHDAWFIFFMAAFAFSNGYLASLCMCFGPKKVKPAEAET
    .****..**.. .*. *...* .**.** **  ** *****.** **..*..* * * *.
NP  LFVPLFMLCHVPQRSRLPILFPQDAYFITFMLLFAVSNGYLVSLTMCLAPRQVLPHEREV

HP  AGAIMAFFLCLGLALGAVFSFLFRAIV
    ***.*.*** ***. ** .****.*..
NP  AGALMTFFLALGLSCGASLSFLFKALL
```

Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. R57372), but it can not be assessed whether these ESTs with partial sequences code for the same protein as the protein of the present invention.

The human nucleolar protein HNP36 has been found as a gene product that plays a role in the growth and multiplication of cells [Williams, J. B. & Lanahan, A. A., Biochem. Biophys. Res. Commun. 213: 325-333 (1995)].

Accordingly, the protein of present invention, which is homologous to said protein, is considered to be a housekeeping protein essential to the growth and multiplication of cells and thereby can be utilized for the diagnosis and the treatment of diseases caused by the abnormality of the present protein.

<HP10297> (Sequence Number 18, 43, 68)

Determination of the whole base sequence for the cDNA insert of clone HP10297 obtained from the human stomach cancer cDNA libraries revealed the structure consisting of a 5'-non-translation region of 62 bp, an ORF of 552 bp, and a 3'-non-translation region of 890 bp. The ORF codes for a protein consisting of 183 amino acid residues with a signal sequence at the N-terminal and one internal transmembrane domain. Therefore, the present protein is considered to be a type-I membrane protein. Figure 21 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. The in vitro translation resulted in the formation of a translation product of 24 kDa that was almost consistent with the molecular weight of 20,574 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was not analogous to any known proteins. Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. R47823), but many sequences are not distinct and the same ORF as that in the present cDNA was not

identified.

<HP10299> (Sequence Number 19, 44, 69)

Determination of the whole base sequence for the cDNA insert of clone HP10299 obtained from the human stomach cancer cDNA libraries revealed the structure consisting of a 5'-non-translation region of 92 bp, an ORF of 351 bp, and a 3'-non-translation region of 89 bp. The ORF codes for a protein consisting of 116 amino acid residues with one transmembrane domain at the N-terminal. Figure 22 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. It was indicated that the present protein remained in the membrane from the observation that the urokinase secretion was not identified upon transduction into the COS7 cells of an expression vector in which a HindIII-VspI fragment (after the Klenow treatment) containing a cDNA fragment encoding the N-terminal 65 amino acid residues in the present protein was inserted at the HindIII-PmaCI site of pSSD3. Therefore, the present protein is considered to be a type-II membrane protein. The in vitro translation resulted in the formation of a translation product of 13 kDa that was almost consistent with the molecular weight of 12,498 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was analogous to the baker's yeast hypothetical membrane protein of 16.5 kDa (SWISS-PROT Accession No. P42834). Table 12 indicates the comparison of the amino acid sequences between the human protein of the present

invention (HP) and the baker's yeast hypothetical membrane protein of 16.5 kDa (SC). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and . represents an amino acid residue analogous to that in the protein of the present invention. The both proteins possessed a homology of 53.0% in the C-terminal region of 66 amino acid residues.

Table 12

```
HP                           MASTVVAVGLTIAAAGFAGRYVLQAMKHMEPQVKQVF

SC   MVLPIIIGLGVTMVALSVKSGLNAWTVYKTLSPLTIAKLNNIRIENPTAGYRDALKFKSS
HP   QSLPKSAFSGGYYRGGFEPKMTKREAALILGVSP----TANKGKIRDAHRRIMLLNHPDK
                 *.***.*.**..** ***..*.      ..  ... **. *. ****.
SC   LIDEELKNRLNQYQGGFAPRMTEPEALLILDISAREINHLDEKLLKKKHRKAMVRNHPDR
HP   GGSPYIAAKINEAKDLLEGQAKK
     *****.********..**
SC   GGSPYMAAKINEAKEVLERSVLLRKR
```

Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. R27748), but many sequences were not distinct and the same ORF as that in the present cDNA was not identified.

<HP10301> (Sequence Number 20, 45, 70)

Determination of the whole base sequence for the cDNA insert of clone HP10301 obtained from the human epidermoid carcinoma cell line KB cDNA libraries revealed the structure consisting of a 5'-non-translation region of 91 bp, an ORF of 459 bp, and a 3'-non-translation region of 112 bp. The ORF codes for a protein consisting of 152 amino acid residues with four transmembrane domains. Figure 23 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. The in vitro translation resulted in the formation of a translation product of 18 kDa that was almost consistent with the molecular weight of 16,516 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was not analogous to any known proteins. Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. N28828), but many sequences were not distinct and the same ORF as that in the present cDNA was not identified.

<HP10302> (Sequence Number 21, 46, 71)

Determination of the whole base sequence for the cDNA insert of clone HP10302 obtained from the human liver cDNA libraries revealed the structure consisting of a 5'-non-translation region of 133 bp, an ORF of 1680 bp, and a 3'-non-translation region of 560 bp. The ORF codes for a protein consisting of 559 amino acid residues with 12

transmembrane domains. Figure 24 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. The in vitro translation did not reveal the formation of distinct bands and revealed the formation of smeary bands at the high-molecular-weight position.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was not analogous to any known proteins. Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. N72434), but they were shorter than the present cDNA and any molecule containing the initiation codon was not identified.

<HP10304> (Sequence Number 22, 47, 72)

Determination of the whole base sequence for the cDNA insert of clone HP10304 obtained from the human osterosarcoma U-2 OS cDNA libraries revealed the structure consisting of a 5'-non-translation region of 10 bp, an ORF of 993 bp, and a 3'-non-translation region of 313 bp. The ORF codes for a protein consisting of 330 amino acid residues with a signal sequence at the N-terminal and one internal transmembrane domain. Therefore, the present protein is considered to be a type-I membrane protein. Figure 25 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. The in vitro translation resulted in the formation of a translation product of 36 kDa that was almost

consistent with the molecular weight of 36,840 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was not analogous to any known proteins. Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. N26840), but the same ORF as that in the present cDNA was not identified.

<HP10305> (Sequence Number 23, 48, 73)

Determination of the whole base sequence for the cDNA insert of clone HP10305 obtained from the human osterosarcoma U-2 OS cDNA libraries revealed the structure consisting of a 5'-non-translation region of 109 bp, an ORF of 327 bp, and a 3'-non-translation region of 457 bp. The ORF codes for a protein consisting of 108 amino acid residues with one transmembrane domain. Figure 26 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. It was indicated that the present protein remained in the membrane from the observation that the urokinase secretion was not identified upon transduction into the COS7 cells of an expression vector in which a HindIII-ApaI fragment (treated with mung-bean nuclease) containing a cDNA fragment encoding the N-terminal 162 amino acid residues in the present protein was inserted at the HindIII-PmaCI site of pSSD3. Therefore, the present protein is considered to be a type-II membrane protein. The in vitro translation resulted

in the formation of a translation product of 15 kDa that was almost consistent with the molecular weight of 12,199 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was not analogous to any known proteins. Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. H02768), but many sequences are not distinct and the same ORF as that in the present cDNA was not identified.

<HP10306> (Sequence Number 24, 49, 74)

Determination of the whole base sequence for the cDNA insert of clone HP10306 obtained from the human osterosarcoma U-2 OS cDNA libraries revealed the structure consisting of a 5'-non-translation region of 229 bp, an ORF of 306 bp, and a 3'-non-translation region of 155 bp. The ORF codes for a protein consisting of 101 amino acid residues with 2 transmembrane domains. Figure 27 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. The in vitro translation resulted in the formation of a translation product of 14 kDa that was almost consistent with the molecular weight of 12,029 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was not analogous to any known proteins. Furthermore, the search of GenBank using the base sequence

of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. H44711), but many sequences are not distinct and the same ORF as that in the present cDNA was not identified.

<HP10328> (Sequence Number 25, 50, 75)

Determination of the whole base sequence for the cDNA insert of clone HP10328 obtained from the human epidermoid carcinoma cell line KB cDNA libraries revealed the structure consisting of a 5'-non-translation region of 117 bp, an ORF of 1119 bp, and a 3'-non-translation region of 950 bp. The ORF codes for a protein consisting of 372 amino acid residues with one transmembrane domain. Figure 28 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. It was indicated that the present protein remained in the membrane from the observation that the urokinase secretion was not identified upon transduction into the COS7 cells of an expression vector in which a HindIII-PmaCI fragment (treated with mung-bean nuclease) containing a cDNA fragment encoding the N-terminal 129 amino acid residues in the present protein was inserted at the HindIII-SmaI site of pSSD3. Therefore, the present protein is considered to be a type-II membrane protein. The in vitro translation resulted in the formation of a translation product of 41 kDa that was almost consistent with the molecular weight of 42,514 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the

protein was analogous to the *Drosophila* neurological secretory signal protein (GenBank Accession No. U41449). Table 13 indicates the comparison of the amino acid sequences between the human protein of the present invention (HP) and the *Drosophila* neurological secretory signal protein (DM). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and . represents an amino acid residue analogous to that in the protein of the present invention. The both proteins possessed a homology of 38.6% in the middle region of 202 amino acid residues.

Table 13

```
HP   MKYLRHRRPNATLILAIGAFTLLLFSLLVSPPTCKVQEQPPAIPEALAWPTPPTRPAPAP

DM                                MQSKHRKLLLRCLLVLPLILLVDYCGLLTHL
HP   CHANTSMVTHPDFATQPQHVQNFLLYRHCRHFPLLQDVPPSKCAQPVFLLLVIKSSPSNY
                                                 **. * ..***. .*
DM   HELNFERHFHYPLNDDTGSGSASSGLDKFAYLRVPSFTAEVPVDQPARLTMLIKSAVGNS
HP   VRRELLRRTWGRERKVRGLQLRLLFLVGTASNPHEARKVNRLLELEAQTHGDILQWDFHD
      *** .***** * . ....** .**.***...  ...*..   *...****** ** *
DM   RRREAIRRTWGYEGRFSDVHLRRVFLLGTAEDS--EKDVAW----ESREHGDILQADFTD
HP   SFFNLTLKQVLFLQWQETRCANASFVLNGDDDVFAHTDNMVFYL----QDHDPGRHLFVG
     ..** *** .* ..*.... ....* *  *** .. ..*.. .*   *.*.*.  **.*
DM   AYFNNTLKTMLGMRWASEQFNRSEFYLFVDDDYYVSAKNVLKFLGRGRQSHQPE-LLFAG
HP   QLIQNVGPIRAFWSKYYVPEVVTQNERYPPYCGGGGFLLSRFTAAALRRAAHVLDIFPID
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   ...* ..*.*  .**.**.     . .*.*** ..*.*.**. .  .*  *.  * .*..*

DM HVFQ-TSPLRHKFSKWYVSLEEYPFDRWPPYVTAGAFILSQKALRQLYAASVHLPLFRFD

HP DVFLGMCLELEGLKPASHSGIRTSGVRAPSQHLSSFDPCFYRDLLLVHRFLPYEMLLMWD

   **.**.

DM DVYLGIVALKAGISLQHCDDFRFHRPAYKGPDSYSSVIASHEFGDPEEMTRVWNECRSAN

HP ALNQPNLTCGNQTQIY


DM YA
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Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. R75815), but they were shorter than the present cDNA and any molecule containing the initiation codon was not identified.

The present invention provides human proteins having transmembrane domains, cDNAs encoding said proteins and eykaryotic cells expressing said cDNA. All of the proteins of the present invention are putative proteins controlling the proliferation and differentiation of the cells, because said proteins exist on the cell membrane. Therefore, the proteins of the present invention can be used as pharmaceuticals or as antigens for preparing antibodies against said proteins. Furthermore, said DNAs can be used for the expression of large amounts of said proteins. The cells expressing large amounts of membrane proteins with transfection of these membrane protein genes can be applied

to the detection of the corresponding ligands, the screening of novel low-molecular medicines, and so on.

In addition to the activities and uses described above, the polynucleotides and proteins of the present invention may exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

Research Uses and Utilities

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel

polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodiesusing DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors

of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., J.

Immunol. 149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Po lyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ, Schreiber, R.D. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 -Nordan, R. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and

Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic

activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial orfungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be

possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration

of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et

al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function in vivo on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis

(see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the commoncold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected ex vivo with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an

MHC class IIα chain protein and an MHC class IIβ chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J.

Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowmanet al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J.J. and Brunswick, M. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify,

among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include,without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995;

Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without

limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss,

Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc.., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced

craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or

other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic

disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin-β group, may be useful as a fertility inducing

therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of

infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis)consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result,such a protein is expected to be useful in treatment of various coagulation disorders (includinghereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular

adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in:Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting

cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of ytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other

factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or caricadic cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating

deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

SEQUENCE LISTING

Sequence No.: 1
Sequence length: 205
Sequence type: Amino acid
Topology: Linear
Sequence kind: Protein
Hypothetical: No
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Fibrosarcoma
  Cell line: HT-1080
  Clone name: HP00442
Sequence description

```
Met Thr Gly Leu Ala Leu Leu Tyr Ser Gly Val Phe Val Ala Phe Trp
 1               5                  10                  15
Ala Cys Ala Leu Ala Val Gly Val Cys Tyr Thr Ile Phe Asp Leu Gly
            20                  25                  30
Phe Arg Phe Asp Val Ala Trp Phe Leu Thr Glu Thr Ser Pro Phe Met
        35                  40                  45
Trp Ser Asn Leu Gly Ile Gly Leu Ala Ile Ser Leu Ser Val Val Gly
    50                  55                  60
Ala Ala Trp Gly Ile Tyr Ile Thr Gly Ser Ser Ile Ile Gly Gly Gly
65                  70                  75                  80
Val Lys Ala Pro Arg Ile Lys Thr Lys Asn Leu Val Ser Ile Ile Phe
                85                  90                  95
Cys Glu Ala Val Ala Ile Tyr Gly Ile Ile Met Ala Ile Val Ile Ser
            100                 105                 110
Asn Met Ala Glu Pro Phe Ser Ala Thr Asp Pro Lys Ala Ile Gly His
        115                 120                 125
Arg Asn Tyr His Ala Gly Tyr Ser Met Phe Gly Ala Gly Leu Thr Val
    130                 135                 140
Gly Leu Ser Asn Leu Phe Cys Gly Val Cys Val Gly Ile Val Gly Ser
145                 150                 155                 160
Gly Ala Ala Leu Ala Asp Ala Gln Asn Pro Ser Leu Phe Val Lys Ile
                165                 170                 175
Leu Ile Val Glu Ile Phe Gly Ser Ala Ile Gly Leu Phe Gly Val Ile
            180                 185                 190
Val Ala Ile Leu Gln Thr Ser Arg Val Lys Met Gly Asp
        195                 200                 205
```

Sequence No.: 2
Sequence length: 371
Sequence type: Amino acid
Topology: Linear
Sequence kind: Protein
Hypothetical: No
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Leukocyte
  Clone name: HP00804
Sequence description

Met Ser His Glu Lys Ser Phe Leu Val Ser Gly Asp Asn Tyr Pro Pro
1 5 10 15
Pro Asn Pro Gly Tyr Pro Gly Gly Pro Gln Pro Pro Met Pro Pro Tyr
20 25 30
Ala Gln Pro Pro Tyr Pro Gly Ala Pro Tyr Pro Gln Pro Pro Phe Gln
35 40 45
Pro Ser Pro Tyr Gly Gln Pro Gly Tyr Pro His Gly Pro Ser Pro Tyr
50 55 60
Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro
65 70 75 80
Gln Gly Pro Tyr Pro Gln Glu Gly Tyr Pro Gln Gly Pro Tyr Pro Gln
85 90 95
Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Ser Pro Phe Pro Pro Asn
100 105 110
Pro Tyr Gly Gln Pro Gln Val Phe Pro Gly Gln Asp Pro Asp Ser Pro
115 120 125
Gln His Gly Asn Tyr Gln Glu Glu Gly Pro Pro Ser Tyr Tyr Asp Asn
130 135 140
Gln Asp Phe Pro Ala Thr Asn Trp Asp Asp Lys Ser Ile Arg Gln Ala
145 150 155 160
Phe Ile Arg Lys Val Phe Leu Val Leu Thr Leu Gln Leu Ser Val Thr
165 170 175
Leu Ser Thr Val Ser Val Phe Thr Phe Val Ala Glu Val Lys Gly Phe
180 185 190
Val Arg Glu Asn Val Trp Thr Tyr Tyr Val Ser Tyr Ala Val Phe Phe
195 200 205
Ile Ser Leu Ile Val Leu Ser Cys Cys Gly Asp Phe Arg Arg Lys His
210 215 220
Pro Trp Asn Leu Val Ala Leu Ser Val Leu Thr Ala Ser Leu Ser Tyr
225 230 235 240
Met Val Gly Met Ile Ala Ser Phe Tyr Asn Thr Glu Ala Val Ile Met
245 250 255

Ala Val Gly Ile Thr Thr Ala Val Cys Phe Thr Val Val Ile Phe Ser
260 265 270

Met Gln Thr Arg Tyr Asp Phe Thr Ser Cys Met Gly Val Leu Leu Val
275 280 285

Ser Met Val Val Leu Phe Ile Phe Ala Ile Leu Cys Ile Phe Ile Arg
290 295 300

Asn Arg Ile Leu Glu Ile Val Tyr Ala Ser Leu Gly Ala Leu Leu Phe
305 310 315 320

Thr Cys Phe Leu Ala Val Asp Thr Gln Leu Leu Leu Gly Asn Lys Gln
325 330 335

Leu Ser Leu Ser Pro Glu Glu Tyr Val Phe Ala Ala Leu Asn Leu Tyr
340 345 350

Thr Asp Ile Ile Asn Ile Phe Leu Tyr Ile Leu Thr Ile Ile Gly Arg
355 360 365

Ala Lys Glu
370

Sequence No.: 3
Sequence length: 179
Sequence type: Amino acid
Topology: Linear
Sequence kind: Protein
Hypothetical: No
Original source:
Organism species: *Homo sapiens*
Cell kind: Stomach cancer
Clone name: HP01098
Sequence description

Met Leu Ser Leu Asp Phe Leu Asp Asp Val Arg Arg Met Asn Lys Arg
1 5 10 15

Gln Leu Tyr Tyr Gln Val Leu Asn Phe Gly Met Ile Val Ser Ser Ala
20 25 30

Leu Met Ile Trp Lys Gly Leu Met Val Ile Thr Gly Ser Glu Ser Pro
35 40 45

Ile Val Val Val Leu Ser Gly Ser Met Glu Pro Ala Phe His Arg Gly
50 55 60

Asp Leu Leu Phe Leu Thr Asn Arg Val Glu Asp Pro Ile Arg Val Gly
65 70 75 80

Glu Ile Val Val Phe Arg Ile Glu Gly Arg Glu Ile Pro Ile Val His
85 90 95

Arg Val Leu Lys Ile His Glu Lys Gln Asn Gly His Ile Lys Phe Leu
100 105 110

Thr Lys Gly Asp Asn Asn Ala Val Asp Asp Arg Gly Leu Tyr Lys Gln
115 120 125
Gly Gln His Trp Leu Glu Lys Lys Asp Val Val Gly Arg Ala Arg Gly
130 135 140
Phe Val Pro Tyr Ile Gly Ile Val Thr Ile Leu Met Asn Asp Tyr Pro
145 150 155 160
Lys Phe Lys Tyr Ala Val Leu Phe Leu Leu Gly Leu Phe Val Leu Val
165 170 175
His Arg Glu

Sequence No.: 4
Sequence length: 347
Sequence type: Amino acid
Topology: Linear
Sequence kind: Protein
Hypothetical: No
Original source:
Organism species: *Homo sapiens*
Cell kind: Liver
Clone name: HP01148
Sequence description

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly
1 5 10 15
Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg
20 25 30
Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val
35 40 45
Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu
50 55 60
Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
65 70 75 80
Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys
85 90 95
Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr
100 105 110
Asp Cys Ser His Glu Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu
115 120 125
Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro
130 135 140
Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr
145 150 155 160
Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys

165 170 175
Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn
180 185 190
Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys
195 200 205
Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly
210 215 220
Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp
225 230 235 240
Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg
245 250 255
Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn
260 265 270
Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly
275 280 285
Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly
290 295 300
Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln
305 310 315 320
Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr
325 330 335
His Gln Glu Asp Val Ala Val Ile Cys Ser Gly
340 345

Sequence No.: 5
Sequence length: 554
Sequence type: Amino acid
Topology: Linear
Sequence kind: Protein
Hypothetical: No
Original source:
Organism species: *Homo sapiens*
Cell kind: Liver
Clone name: HP01293
Sequence description

Met Pro Thr Val Asp Asp Ile Leu Glu Gln Val Gly Glu Ser Gly Trp
1 5 10 15
Phe Gln Lys Gln Ala Phe Leu Ile Leu Cys Leu Leu Ser Ala Ala Phe
20 25 30
Ala Pro Ile Cys Val Gly Ile Val Phe Leu Gly Phe Thr Pro Asp His
35 40 45
His Cys Gln Ser Pro Gly Val Ala Glu Leu Ser Gln Arg Cys Gly Trp

50 55 60
Ser Pro Ala Glu Glu Leu Asn Tyr Thr Val Pro Gly Leu Gly Pro Ala
65 70 75 80
Gly Glu Ala Phe Leu Gly Gln Cys Arg Arg Tyr Glu Val Asp Trp Asn
85 90 95
Gln Ser Ala Leu Ser Cys Val Asp Pro Leu Ala Ser Leu Ala Thr Asn
100 105 110
Arg Ser His Leu Pro Leu Gly Pro Cys Gln Asp Gly Trp Val Tyr Asp
115 120 125
Thr Pro Gly Ser Ser Ile Val Thr Glu Phe Asn Leu Val Cys Ala Asp
130 135 140
Ser Trp Lys Leu Asp Leu Phe Gln Ser Cys Leu Asn Ala Gly Phe Phe
145 150 155 160
Phe Gly Ser Leu Gly Val Gly Tyr Phe Ala Asp Arg Phe Gly Arg Lys
165 170 175
Leu Cys Leu Leu Gly Thr Val Leu Val Asn Ala Val Ser Gly Val Leu
180 185 190
Met Ala Phe Ser Pro Asn Tyr Met Ser Met Leu Leu Phe Arg Leu Leu
195 200 205
Gln Gly Leu Val Ser Lys Gly Asn Trp Met Ala Gly Tyr Thr Leu Ile
210 215 220
Thr Glu Phe Val Gly Ser Gly Ser Arg Arg Thr Val Ala Ile Met Tyr
225 230 235 240
Gln Met Ala Phe Thr Val Gly Leu Val Ala Leu Thr Gly Leu Ala Tyr
245 250 255
Ala Leu Pro His Trp Arg Trp Leu Gln Leu Ala Val Ser Leu Pro Thr
260 265 270
Phe Leu Phe Leu Leu Tyr Tyr Trp Cys Val Pro Glu Ser Pro Arg Trp
275 280 285
Leu Leu Ser Gln Lys Arg Asn Thr Glu Ala Ile Lys Ile Met Asp His
290 295 300
Ile Ala Gln Lys Asn Gly Lys Leu Pro Pro Ala Asp Leu Lys Met Leu
305 310 315 320
Ser Leu Glu Glu Asp Val Thr Glu Lys Leu Ser Pro Ser Phe Ala Asp
325 330 335
Leu Phe Arg Thr Pro Arg Leu Arg Lys Arg Thr Phe Ile Leu Met Tyr
340 345 350
Leu Trp Phe Thr Asp Ser Val Leu Tyr Gln Gly Leu Ile Leu His Met
355 360 365
Gly Ala Thr Ser Gly Asn Leu Tyr Leu Asp Phe Leu Tyr Ser Ala Leu
370 375 380
Val Glu Ile Pro Gly Ala Phe Ile Ala Leu Ile Thr Ile Asp Arg Val
385 390 395 400
Gly Arg Ile Tyr Pro Met Ala Val Ser Asn Leu Leu Ala Gly Ala Ala

405 410 415
Cys Leu Val Met Ile Phe Ile Ser Pro Asp Leu His Trp Leu Asn Ile
420 425 430
Ile Ile Met Cys Val Gly Arg Met Gly Ile Thr Ile Ala Ile Gln Met
435 440 445
Ile Cys Leu Val Asn Ala Glu Leu Tyr Pro Thr Phe Val Arg Asn Leu
450 455 460
Gly Val Met Val Cys Ser Ser Leu Cys Asp Ile Gly Gly Ile Ile Thr
465 470 475 480
Pro Phe Ile Val Phe Arg Leu Arg Glu Val Trp Gln Ala Leu Pro Leu
485 490 495
Ile Leu Phe Ala Val Leu Gly Leu Leu Ala Ala Gly Val Thr Leu Leu
500 505 510
Leu Pro Glu Thr Lys Gly Val Ala Leu Pro Glu Thr Met Lys Asp Ala
515 520 525
Glu Asn Leu Gly Arg Lys Ala Lys Pro Lys Glu Asn Thr Ile Tyr Leu
530 535 540
Lys Val Gln Thr Ser Glu Pro Ser Gly Thr
545 550

Sequence No.: 6
Sequence length: 350
Sequence type: Amino acid
Topology: Linear
Sequence kind: Protein
Hypothetical: No
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Epidermoid carcinoma
  Cell line: KB
  Clone name: HP10013
Sequence description

Met Ala Val Phe Val Val Leu Leu Ala Leu Val Ala Gly Val Leu Gly
1 5 10 15
Asn Glu Phe Ser Ile Leu Lys Ser Pro Gly Ser Val Val Phe Arg Asn
20 25 30
Gly Asn Trp Pro Ile Pro Gly Glu Arg Ile Pro Asp Val Ala Ala Leu
35 40 45
Ser Met Gly Phe Ser Val Lys Glu Asp Leu Ser Trp Pro Gly Leu Ala
50 55 60
Val Gly Asn Leu Phe His Arg Pro Arg Ala Thr Val Met Val Met Val
65 70 75 80

Lys Gly Val Asn Lys Leu Ala Leu Pro Pro Gly Ser Val Ile Ser Tyr
                85   90   95
Pro Leu Glu Asn Ala Val Pro Phe Ser Leu Asp Ser Val Ala Asn Ser
            100   105   110
Ile His Ser Leu Phe Ser Glu Glu Thr Pro Val Val Leu Gln Leu Ala
        115   120   125
Pro Ser Glu Glu Arg Val Tyr Met Val Gly Lys Ala Asn Ser Val Phe
    130   135   140
Glu Asp Leu Ser Val Thr Leu Arg Gln Leu Arg Asn Arg Leu Phe Gln
145   150   155   160
Glu Asn Ser Val Leu Ser Ser Leu Pro Leu Asn Ser Leu Ser Arg Asn
                165   170   175
Asn Glu Val Asp Leu Leu Phe Leu Ser Glu Leu Gln Val Leu His Asp
            180   185   190
Ile Ser Ser Leu Leu Ser Arg His Lys His Leu Ala Lys Asp His Ser
        195   200   205
Pro Asp Leu Tyr Ser Leu Glu Leu Ala Gly Leu Asp Glu Ile Gly Lys
    210   215   220
Arg Tyr Gly Glu Asp Ser Glu Gln Phe Arg Asp Ala Ser Lys Ile Leu
225   230   235   240
Val Asp Ala Leu Gln Lys Phe Ala Asp Asp Met Tyr Ser Leu Tyr Gly
                245   250   255
Gly Asn Ala Val Val Glu Leu Val Thr Val Lys Ser Phe Asp Thr Ser
            260   265   270
Leu Ile Arg Lys Thr Arg Thr Ile Leu Glu Ala Lys Gln Ala Lys Asn
        275   280   285
Pro Ala Ser Pro Tyr Asn Leu Ala Tyr Lys Tyr Asn Phe Glu Tyr Ser
    290   295   300
Val Val Phe Asn Met Val Leu Trp Ile Met Ile Ala Leu Ala Leu Ala
305   310   315   320
Val Ile Ile Thr Ser Tyr Asn Ile Trp Asn Met Asp Pro Gly Tyr Asp
                325   330   335
Ser Ile Ile Tyr Arg Met Thr Asn Gln Lys Ile Arg Met Asp
            340   345   350

Sequence No.: 7
Sequence length: 209
Sequence type: Amino acid
Topology: Linear
Sequence kind: Protein
Hypothetical: No
Original source:
  Organism species: *Homo sapiens*

Cell kind: Fibrosarcoma
Cell line: HT-1080
Clone name: HP10034
Sequence description

Met Val Ser Ser Pro Cys Thr Gln Ala Ser Ser Arg Thr Cys Ser Arg
1 5 10 15
Ile Leu Gly Leu Ser Leu Gly Thr Ala Ala Leu Phe Ala Ala Gly Ala
20 25 30
Asn Val Ala Leu Leu Leu Pro Asn Trp Asp Val Thr Tyr Leu Leu Arg
35 40 45
Gly Leu Leu Gly Arg His Ala Met Leu Gly Thr Gly Leu Trp Gly Gly
50 55 60
Gly Leu Met Val Leu Thr Ala Ala Ile Leu Ile Ser Leu Met Gly Trp
65 70 75 80
Arg Tyr Gly Cys Phe Ser Lys Ser Gly Leu Cys Arg Ser Val Leu Thr
85 90 95
Ala Leu Leu Ser Gly Gly Leu Ala Leu Leu Gly Ala Leu Ile Cys Phe
100 105 110
Val Thr Ser Gly Val Ala Leu Lys Asp Gly Pro Phe Cys Met Phe Asp
115 120 125
Val Ser Ser Phe Asn Gln Thr Gln Ala Trp Lys Tyr Gly Tyr Pro Phe
130 135 140
Lys Asp Leu His Ser Arg Asn Tyr Leu Tyr Asp Arg Ser Leu Trp Asn
145 150 155 160
Ser Val Cys Leu Glu Pro Ser Ala Ala Val Val Trp His Val Ser Leu
165 170 175
Phe Ser Ala Leu Leu Cys Ile Ser Leu Leu Gln Leu Leu Leu Val Val
180 185 190
Val His Val Ile Asn Ser Leu Leu Gly Leu Phe Cys Ser Leu Cys Glu
195 200 205
Lys

Sequence No.: 8
Sequence length: 163
Sequence type: Amino acid
Topology: Linear
Sequence kind: Protein
Hypothetical: No
Original source:
Organism species: *Homo sapiens*
Cell kind: Fibrosarcoma
Cell line: HT-1080

Clone name: HP10050

Sequence description

Met Ala Ala Gly Leu Phe Gly Leu Ser Ala Arg Arg Leu Leu Ala Ala
1 5 10 15
Ala Ala Thr Arg Gly Leu Pro Ala Ala Arg Val Arg Trp Glu Ser Ser
20 25 30
Phe Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala Gly Lys Arg Pro
35 40 45
Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu Pro Glu Asp Glu
50 55 60
Asn Leu Tyr Glu Lys Asn Pro Asp Ser His Gly Tyr Asp Lys Asp Pro
65 70 75 80
Val Leu Asp Val Trp Asn Met Arg Leu Val Phe Phe Phe Gly Val Ser
85 90 95
Ile Ile Leu Val Leu Gly Ser Thr Phe Val Ala Tyr Leu Pro Asp Tyr
100 105 110
Arg Cys Thr Gly Cys Pro Arg Ala Trp Asp Gly Met Lys Glu Trp Ser
115 120 125
Arg Arg Glu Ala Glu Arg Leu Val Lys Tyr Arg Glu Ala Asn Gly Leu
130 135 140
Pro Ile Met Glu Ser Asn Cys Phe Asp Pro Ser Lys Ile Gln Leu Pro
145 150 155 160
Glu Asp Glu

Sequence No.: 9

Sequence length: 92

Sequence type: Amino acid

Topology: Linear

Sequence kind: Protein

Hypothetical: No

Original source:

Organism species: *Homo sapiens*

Cell kind: Stomach cancer

Clone name: HP10071

Sequence description

Met Thr Lys Leu Ala Gln Trp Leu Trp Gly Leu Ala Ile Leu Gly Ser
1 5 10 15
Thr Trp Val Ala Leu Thr Thr Gly Ala Leu Gly Leu Glu Leu Pro Leu
20 25 30
Ser Cys Gln Glu Val Leu Trp Pro Leu Pro Ala Tyr Leu Leu Val Ser
35 40 45

Ala Gly Cys Tyr Ala Leu Gly Thr Val Gly Tyr Arg Val Ala Thr Phe
50 55 60
His Asp Cys Glu Asp Ala Ala Arg Glu Leu Gln Ser Gln Ile Gln Glu
65 70 75 80
Ala Arg Ala Asp Leu Ala Arg Arg Gly Leu Arg Phe
85 90

Sequence No.: 10
Sequence length: 172
Sequence type: Amino acid
Topology: Linear
Sequence kind: Protein
Hypothetical: No
Original source:
Organism species: *Homo sapiens*
Cell kind: Lymphoma
Cell line: U937
Clone name: HP10076
Sequence description

Met Glu Tyr Leu Ala His Pro Ser Thr Leu Gly Leu Ala Val Gly Val
1 5 10 15
Ala Cys Gly Met Cys Leu Gly Trp Ser Leu Arg Val Cys Phe Gly Met
20 25 30
Leu Pro Lys Ser Lys Thr Ser Lys Thr His Thr Asp Thr Glu Ser Glu
35 40 45
Ala Ser Ile Leu Gly Asp Ser Gly Glu Tyr Lys Met Ile Leu Val Val
50 55 60
Arg Asn Asp Leu Lys Met Gly Lys Gly Lys Val Ala Ala Gln Cys Ser
65 70 75 80
His Ala Ala Val Ser Ala Tyr Lys Gln Ile Gln Arg Arg Asn Pro Glu
85 90 95
Met Leu Lys Gln Trp Glu Tyr Cys Gly Gln Pro Lys Val Val Val Lys
100 105 110
Ala Pro Asp Glu Glu Thr Leu Ile Ala Leu Leu Ala His Ala Lys Met
115 120 125
Leu Gly Leu Thr Val Ser Leu Ile Gln Asp Ala Gly Arg Thr Gln Ile
130 135 140
Ala Pro Gly Ser Gln Thr Val Leu Gly Ile Gly Pro Gly Pro Ala Asp
145 150 155 160
Leu Ile Asp Lys Val Thr Gly His Leu Lys Leu Tyr
165 170

Sequence No.: 11
Sequence length: 149
Sequence type: Amino acid
Topology: Linear
Sequence kind: Protein
Hypothetical: No
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Lymphoma
  Cell line: U937
  Clone name: HP10085
Sequence description

```
Met Met Thr Lys His Lys Lys Cys Phe Ile Ile Val Gly Val Leu Ile
 1               5                  10                  15
Thr Thr Asn Ile Ile Thr Leu Ile Val Lys Leu Thr Arg Asp Ser Gln
            20                  25                  30
Ser Leu Cys Pro Tyr Asp Trp Ile Gly Phe Gln Asn Lys Cys Tyr Tyr
        35                  40                  45
Phe Ser Lys Glu Glu Gly Asp Trp Asn Ser Ser Lys Tyr Asn Cys Ser
    50                  55                  60
Thr Gln His Ala Asp Leu Thr Ile Ile Asp Asn Ile Glu Glu Met Asn
65                  70                  75                  80
Phe Leu Arg Arg Tyr Lys Cys Ser Ser Asp His Trp Ile Gly Leu Lys
                85                  90                  95
Met Ala Lys Asn Arg Thr Gly Gln Trp Val Asp Gly Ala Thr Phe Thr
            100                 105                 110
Lys Ser Phe Gly Met Arg Gly Ser Glu Gly Cys Ala Tyr Leu Ser Asp
        115                 120                 125
Asp Gly Ala Ala Thr Ala Arg Cys Tyr Thr Glu Arg Lys Trp Ile Cys
    130                 135                 140
Arg Lys Arg Ile His
145
```

Sequence No.: 12
Sequence length: 188
Sequence type: Amino acid
Topology: Linear
Sequence kind: Protein
Hypothetical: No
Original source:
  Organism species: *Homo sapiens*

Cell kind: Stomach cancer
Clone name: HP10122
Sequence description

Met Ser Thr Met Phe Ala Asp Thr Leu Leu Ile Val Phe Ile Ser Val
1 5 10 15
Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp Val Leu Val Tyr Arg
20 25 30
Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val Glu Lys Gln Ser Lys
35 40 45
Lys Leu Glu Lys Lys Lys Glu Thr Ile Thr Glu Ser Ala Gly Arg Gln
50 55 60
Gln Lys Lys Lys Ile Glu Arg Gln Glu Glu Lys Leu Lys Asn Asn Asn
65 70 75 80
Arg Asp Leu Ser Met Val Arg Met Lys Ser Met Phe Ala Ile Gly Phe
85 90 95
Cys Phe Thr Ala Leu Met Gly Met Phe Asn Ser Ile Phe Asp Gly Arg
100 105 110
Val Val Ala Lys Leu Pro Phe Thr Pro Leu Ser Tyr Ile Gln Gly Leu
115 120 125
Ser His Arg Asn Leu Leu Gly Asp Asp Thr Thr Asp Cys Ser Phe Ile
130 135 140
Phe Leu Tyr Ile Leu Cys Thr Met Ser Ile Arg Gln Asn Ile Gln Lys
145 150 155 160
Ile Leu Gly Leu Ala Pro Ser Arg Ala Ala Thr Lys Gln Ala Gly Gly
165 170 175
Phe Leu Gly Pro Pro Pro Pro Ser Gly Lys Phe Ser
180 185

Sequence No.: 13
Sequence length: 215
Sequence type: Amino acid
Topology: Linear
Sequence kind: Protein
Hypothetical: No
Original source:
Organism species: *Homo sapiens*
Cell kind: Lymphoma
Cell line: U937
Clone name: HP10136
Sequence description

Met Val Leu Leu Thr Met Ile Ala Arg Val Ala Asp Gly Leu Pro Leu

```
                 1               5                  10                  15
Ala Ala Ser Met Gln Glu Asp Glu Gln Ser Gly Arg Asp Leu Gln Gln
                20                  25                  30
Tyr Gln Ser Gln Ala Lys Gln Leu Phe Arg Lys Leu Asn Glu Gln Ser
            35                  40                  45
Pro Thr Arg Cys Thr Leu Glu Ala Gly Ala Met Thr Phe His Tyr Ile
        50                  55                  60
Ile Glu Gln Gly Val Cys Tyr Leu Val Leu Cys Glu Ala Ala Phe Pro
 65                 70                  75                  80
Lys Lys Leu Ala Phe Ala Tyr Leu Glu Asp Leu His Ser Glu Phe Asp
                    85                  90                  95
Glu Gln His Gly Lys Lys Val Pro Thr Val Ser Arg Pro Tyr Ser Phe
                100                 105                 110
Ile Glu Phe Asp Thr Phe Ile Gln Lys Thr Lys Lys Leu Tyr Ile Asp
            115                 120                 125
Ser Arg Ala Arg Arg Asn Leu Gly Ser Ile Asn Thr Glu Leu Gln Asp
        130                 135                 140
Val Gln Arg Ile Met Val Ala Asn Ile Glu Glu Val Leu Gln Arg Gly
145                 150                 155                 160
Glu Ala Leu Ser Ala Leu Asp Ser Lys Ala Asn Asn Leu Ser Ser Leu
                    165                 170                 175
Ser Lys Lys Tyr Arg Gln Asp Ala Lys Tyr Leu Asn Met Arg Ser Thr
                180                 185                 190
Tyr Ala Lys Leu Ala Ala Val Ala Val Phe Phe Ile Met Leu Ile Val
            195                 200                 205
Tyr Val Arg Phe Trp Trp Leu
        210                 215
```

Sequence No.: 14
Sequence length: 112
Sequence type: Amino acid
Topology: Linear
Sequence kind: Protein
Hypothetical: No
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Stomach cancer
  Clone name: HP10175
Sequence description

```
Met Gln Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly Phe Gly
  1               5                  10                  15
Tyr Ala Ala Leu Val Ala Ser Gly Gly Ile Ile Gly Tyr Val Lys Ala
```

20 25 30

Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu Ala

35 40 45

Gly Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val Trp Val

50 55 60

Phe Leu Ala Thr Ser Gly Thr Leu Ala Gly Ile Met Gly Met Arg Phe

65 70 75 80

Tyr His Ser Gly Lys Phe Met Pro Ala Gly Leu Ile Ala Gly Ala Ser

85 90 95

Leu Leu Met Val Ala Lys Val Gly Val Ser Met Phe Asn Arg Pro His

100 105 110

Sequence No.: 15
Sequence length: 114
Sequence type: Amino acid
Topology: Linear
Sequence kind: Protein
Hypothetical: No
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Epidermoid carcinoma
  Cell line: KB
  Clone name: HP10179
Sequence description

Met Glu Lys Pro Leu Phe Pro Leu Val Pro Leu His Trp Phe Gly Phe

1 5 10 15

Gly Tyr Thr Ala Leu Val Val Ser Gly Gly Ile Val Gly Tyr Val Lys

20 25 30

Thr Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu

35 40 45

Ala Gly Leu Gly Ala Tyr Gln Leu Tyr Gln Asp Pro Arg Asn Val Trp

50 55 60

Gly Phe Leu Ala Ala Thr Ser Val Thr Phe Val Gly Val Met Gly Met

65 70 75 80

Arg Ser Tyr Tyr Tyr Gly Lys Phe Met Pro Val Gly Leu Ile Ala Gly

85 90 95

Ala Ser Leu Leu Met Ala Ala Lys Val Gly Val Arg Met Leu Met Thr

100 105 110

Ser Asp

Sequence No.: 16

Sequence length: 327
Sequence type: Amino acid
Topology: Linear
Sequence kind: Protein
Hypothetical: No
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Fibrosarcoma
  Cell line: HT-1080
  Clone name: HP10196
Sequence description

```
Met Ala Ala Ala Ala Ala Ala Ala Ala Ala Thr Asn Gly Thr Gly Gly
 1               5                  10                  15
Ser Ser Gly Met Glu Val Asp Ala Ala Val Val Pro Ser Val Met Ala
            20                  25                  30
Cys Gly Val Thr Gly Ser Val Ser Val Ala Leu His Pro Leu Val Ile
        35                  40                  45
Leu Asn Ile Ser Asp His Trp Ile Arg Met Arg Ser Gln Glu Gly Arg
    50                  55                  60
Pro Val Gln Val Ile Gly Ala Leu Ile Gly Lys Gln Glu Gly Arg Asn
65                  70                  75                  80
Ile Glu Val Met Asn Ser Phe Glu Leu Leu Ser His Thr Val Glu Glu
                85                  90                  95
Lys Ile Ile Ile Asp Lys Glu Tyr Tyr Tyr Thr Lys Glu Glu Gln Phe
            100                 105                 110
Lys Gln Val Phe Lys Glu Leu Glu Phe Leu Gly Trp Tyr Thr Thr Gly
        115                 120                 125
Gly Pro Pro Asp Pro Ser Asp Ile His Val His Lys Gln Val Cys Glu
    130                 135                 140
Ile Ile Glu Ser Pro Leu Phe Leu Lys Leu Asn Pro Met Thr Lys His
145                 150                 155                 160
Thr Asp Leu Pro Val Ser Val Phe Glu Ser Val Ile Asp Ile Ile Asn
                165                 170                 175
Gly Glu Ala Thr Met Leu Phe Ala Glu Leu Thr Tyr Thr Leu Ala Thr
            180                 185                 190
Glu Glu Ala Glu Arg Ile Gly Val Asp His Val Ala Arg Met Thr Ala
        195                 200                 205
Thr Gly Ser Gly Glu Asn Ser Thr Val Ala Glu His Leu Ile Ala Gln
    210                 215                 220
His Ser Ala Ile Lys Met Leu His Ser Arg Val Lys Leu Ile Leu Glu
225                 230                 235                 240
Tyr Val Lys Ala Ser Glu Ala Gly Glu Val Pro Phe Asn His Glu Ile
                245                 250                 255
```

Leu Arg Glu Ala Tyr Ala Leu Cys His Cys Leu Pro Val Leu Ser Thr
260 265 270
Asp Lys Phe Lys Thr Asp Phe Tyr Asp Gln Cys Asn Asp Val Gly Leu
275 280 285
Met Ala Tyr Leu Gly Thr Ile Thr Lys Thr Cys Asn Thr Met Asn Gln
290 295 300
Phe Val Asn Lys Phe Asn Val Leu Tyr Asp Arg Gln Gly Ile Gly Arg
305 310 315 320
Arg Met Arg Gly Leu Phe Phe
325

Sequence No.: 17
Sequence length: 373
Sequence type: Amino acid
Topology: Linear
Sequence kind: Protein
Hypothetical: No
Original source:
Organism species: *Homo sapiens*
Cell kind: Fibrosarcoma
Cell line: HT-1080
Clone name: HP10235
Sequence description

Met Thr Leu Cys Ala Met Leu Pro Leu Leu Leu Phe Thr Tyr Leu Asn
1 5 10 15
Ser Phe Leu His Gln Arg Ile Pro Gln Ser Val Arg Ile Leu Gly Ser
20 25 30
Leu Val Ala Ile Leu Leu Val Phe Leu Ile Thr Ala Ile Leu Val Lys
35 40 45
Val Gln Leu Asp Ala Leu Pro Phe Phe Val Ile Thr Met Ile Lys Ile
50 55 60
Val Leu Ile Asn Ser Phe Gly Ala Ile Leu Gln Gly Ser Leu Phe Gly
65 70 75 80
Leu Ala Gly Leu Leu Pro Ala Ser Tyr Thr Ala Pro Ile Met Ser Gly
85 90 95
Gln Gly Leu Ala Gly Phe Phe Ala Ser Val Ala Met Ile Cys Ala Ile
100 105 110
Ala Ser Gly Ser Glu Leu Ser Glu Ser Ala Phe Gly Tyr Phe Ile Thr
115 120 125
Ala Cys Ala Val Ile Ile Leu Thr Ile Ile Cys Tyr Leu Gly Leu Pro
130 135 140
Arg Leu Glu Phe Tyr Arg Tyr Tyr Gln Gln Leu Lys Leu Glu Gly Pro

145 150 155 160
Gly Glu Gln Glu Thr Lys Leu Asp Leu Ile Ser Lys Gly Glu Glu Pro
165 170 175
Arg Ala Gly Lys Glu Glu Ser Gly Val Ser Val Ser Asn Ser Gln Pro
180 185 190
Thr Asn Glu Ser His Ser Ile Lys Ala Ile Leu Lys Asn Ile Ser Val
195 200 205
Leu Ala Phe Ser Val Cys Phe Ile Phe Thr Ile Thr Ile Gly Met Phe
210 215 220
Pro Ala Val Thr Val Glu Val Lys Ser Ser Ile Ala Gly Ser Ser Thr
225 230 235 240
Trp Glu Arg Tyr Phe Ile Pro Val Ser Cys Phe Leu Thr Phe Asn Ile
245 250 255
Phe Asp Trp Leu Gly Arg Ser Leu Thr Ala Val Phe Met Trp Pro Gly
260 265 270
Lys Asp Ser Arg Trp Leu Pro Ser Leu Val Leu Ala Arg Leu Val Phe
275 280 285
Val Pro Leu Leu Leu Leu Cys Asn Ile Lys Pro Arg Arg Tyr Leu Thr
290 295 300
Val Val Phe Glu His Asp Ala Trp Phe Ile Phe Phe Met Ala Ala Phe
305 310 315 320
Ala Phe Ser Asn Gly Tyr Leu Ala Ser Leu Cys Met Cys Phe Gly Pro
325 330 335
Lys Lys Val Lys Pro Ala Glu Ala Glu Thr Ala Gly Ala Ile Met Ala
340 345 350
Phe Phe Leu Cys Leu Gly Leu Ala Leu Gly Ala Val Phe Ser Phe Leu
355 360 365
Phe Arg Ala Ile Val
370

Sequence No.: 18
Sequence length: 183
Sequence type: Amino acid
Topology: Linear
Sequence kind: Protein
Hypothetical: No
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Stomach cancer
  Clone name: HP10297
Sequence description

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
1 5 10 15
Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile
20 25 30
Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
35 40 45
Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
50 55 60
Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
65 70 75 80
Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
85 90 95
Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
100 105 110
Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
115 120 125
Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala Ser
130 135 140
Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
145 150 155 160
Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
165 170 175
Asp Arg His Lys Met Leu Ser
180

Sequence No.: 19
Sequence length: 116
Sequence type: Amino acid
Topology: Linear
Sequence kind: Protein
Hypothetical: No
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Stomach cancer
  Clone name: HP10299
Sequence description

Met Ala Ser Thr Val Val Ala Val Gly Leu Thr Ile Ala Ala Ala Gly
1 5 10 15
Phe Ala Gly Arg Tyr Val Leu Gln Ala Met Lys His Met Glu Pro Gln
20 25 30
Val Lys Gln Val Phe Gln Ser Leu Pro Lys Ser Ala Phe Ser Gly Gly
35 40 45

Tyr Tyr Arg Gly Gly Phe Glu Pro Lys Met Thr Lys Arg Glu Ala Ala
50 55 60

Leu Ile Leu Gly Val Ser Pro Thr Ala Asn Lys Gly Lys Ile Arg Asp
65 70 75 80

Ala His Arg Arg Ile Met Leu Leu Asn His Pro Asp Lys Gly Gly Ser
85 90 95

Pro Tyr Ile Ala Ala Lys Ile Asn Glu Ala Lys Asp Leu Leu Glu Gly
100 105 110

Gln Ala Lys Lys
115

Sequence No.: 20
Sequence length: 152
Sequence type: Amino acid
Topology: Linear
Sequence kind: Protein
Hypothetical: No
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Epidermoid carcinoma
  Cell line: KB
  Clone name: HP10301
Sequence description

Met Ala Val Leu Ser Lys Glu Tyr Gly Phe Val Leu Leu Thr Gly Ala
1 5 10 15

Ala Ser Phe Ile Met Val Ala His Leu Ala Ile Asn Val Ser Lys Ala
20 25 30

Arg Lys Lys Tyr Lys Val Glu Tyr Pro Ile Met Tyr Ser Thr Asp Pro
35 40 45

Glu Asn Gly His Ile Phe Asn Cys Ile Gln Arg Ala His Gln Asn Thr
50 55 60

Leu Glu Val Tyr Pro Pro Phe Leu Phe Phe Leu Ala Val Gly Gly Val
65 70 75 80

Tyr His Pro Arg Ile Ala Ser Gly Leu Gly Leu Ala Trp Ile Val Gly
85 90 95

Arg Val Leu Tyr Ala Tyr Gly Tyr Tyr Thr Gly Glu Pro Ser Lys Arg
100 105 110

Ser Arg Gly Ala Leu Gly Ser Ile Ala Leu Leu Gly Leu Val Gly Thr
115 120 125

Thr Val Cys Ser Ala Phe Gln His Leu Gly Trp Val Lys Ser Gly Leu
130 135 140

Gly Ser Gly Pro Lys Cys Cys His

145 150

Sequence No.: 21
Sequence length: 559
Sequence type: Amino acid
Topology: Linear
Sequence kind: Protein
Hypothetical: No
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Liver
  Clone name: HP10302
Sequence description

Met Ala Pro Thr Leu Gln Gln Ala Tyr Arg Arg Arg Trp Trp Met Ala
1 5 10 15
Cys Thr Ala Val Leu Glu Asn Leu Phe Phe Ser Ala Val Leu Leu Gly
20 25 30
Trp Gly Ser Leu Leu Ile Ile Leu Lys Asn Glu Gly Phe Tyr Ser Ser
35 40 45
Thr Cys Pro Ala Glu Ser Ser Thr Asn Thr Thr Gln Asp Glu Gln Arg
50 55 60
Arg Trp Pro Gly Cys Asp Gln Gln Asp Glu Met Leu Asn Leu Gly Phe
65 70 75 80
Thr Ile Gly Ser Phe Val Leu Ser Ala Thr Thr Leu Pro Leu Gly Ile
85 90 95
Leu Met Asp Arg Phe Gly Pro Arg Pro Val Arg Leu Val Gly Ser Ala
100 105 110
Cys Phe Thr Ala Ser Cys Thr Leu Met Ala Leu Ala Ser Arg Asp Val
115 120 125
Glu Ala Leu Ser Pro Leu Ile Phe Leu Ala Leu Ser Leu Asn Gly Phe
130 135 140
Gly Gly Ile Cys Leu Thr Phe Thr Ser Leu Thr Leu Pro Asn Met Phe
145 150 155 160
Gly Asn Leu Arg Ser Thr Leu Met Ala Leu Met Ile Gly Ser Tyr Ala
165 170 175
Ser Ser Ala Ile Thr Phe Pro Gly Ile Lys Leu Ile Tyr Asp Ala Gly
180 185 190
Val Ala Phe Val Val Ile Met Phe Thr Trp Ser Gly Leu Ala Cys Leu
195 200 205
Ile Phe Leu Asn Cys Thr Leu Asn Trp Pro Ile Glu Ala Phe Pro Ala
210 215 220
Pro Glu Glu Val Asn Tyr Thr Lys Lys Ile Lys Leu Ser Gly Leu Ala

225 230 235 240

Leu Asp His Lys Val Thr Gly Asp Leu Phe Tyr Thr His Val Thr Thr

245 250 255

Met Gly Gln Arg Leu Ser Gln Lys Ala Pro Ser Leu Glu Asp Gly Ser

260 265 270

Asp Ala Phe Met Ser Pro Gln Asp Val Arg Gly Thr Ser Glu Asn Leu

275 280 285

Pro Glu Arg Ser Val Pro Leu Arg Lys Ser Leu Cys Ser Pro Thr Phe

290 295 300

Leu Trp Ser Leu Leu Thr Met Gly Met Thr Gln Leu Arg Ile Ile Phe

305 310 315 320

Tyr Met Ala Ala Val Asn Lys Met Leu Glu Tyr Leu Val Thr Gly Gly

325 330 335

Gln Glu His Glu Thr Asn Glu Gln Gln Gln Lys Val Ala Glu Thr Val

340 345 350

Gly Phe Tyr Ser Ser Val Phe Gly Ala Met Gln Leu Leu Cys Leu Leu

355 360 365

Thr Cys Pro Leu Ile Gly Tyr Ile Met Asp Trp Arg Ile Lys Asp Cys

370 375 380

Val Asp Ala Pro Thr Gln Gly Thr Val Leu Gly Asp Ala Arg Asp Gly

385 390 395 400

Val Ala Thr Lys Ser Ile Arg Pro Arg Tyr Cys Lys Ile Gln Lys Leu

405 410 415

Thr Asn Ala Ile Ser Ala Phe Thr Leu Thr Asn Leu Leu Leu Val Gly

420 425 430

Phe Gly Ile Thr Cys Leu Ile Asn Asn Leu His Leu Gln Phe Val Thr

435 440 445

Phe Val Leu His Thr Ile Val Arg Gly Phe Phe His Ser Ala Cys Gly

450 455 460

Ser Leu Tyr Ala Ala Val Phe Pro Ser Asn His Phe Gly Thr Leu Thr

465 470 475 480

Gly Leu Gln Ser Leu Ile Ser Ala Val Phe Ala Leu Leu Gln Gln Pro

485 490 495

Leu Phe Met Ala Met Val Gly Pro Leu Lys Gly Glu Pro Phe Trp Val

500 505 510

Asn Leu Gly Leu Leu Leu Phe Ser Leu Leu Gly Phe Leu Leu Pro Ser

515 520 525

Tyr Leu Phe Tyr Tyr Arg Ala Arg Leu Gln Gln Glu Tyr Ala Ala Asn

530 535 540

Gly Met Gly Pro Leu Lys Val Leu Ser Gly Ser Glu Val Thr Ala

545 550 555

Sequence No.: 22

Sequence length: 330
Sequence type: Amino acid
Topology: Linear
Sequence kind: Protein
Hypothetical: No
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Osterosarcoma
  Cell line: U-2 OS
  Clone name: HP10304
Sequence description

Met Glu Gly Ala Pro Pro Gly Ser Leu Ala Leu Arg Leu Leu Leu Phe
1 5 10 15
Val Ala Leu Pro Ala Ser Gly Trp Leu Thr Thr Gly Ala Pro Glu Pro
20 25 30
Pro Pro Leu Ser Gly Ala Pro Gln Asp Gly Ile Arg Ile Asn Val Thr
35 40 45
Thr Leu Lys Asp Asp Gly Asp Ile Ser Lys Gln Gln Val Val Leu Asn
50 55 60
Ile Thr Tyr Glu Ser Gly Gln Val Tyr Val Asn Asp Leu Pro Val Asn
65 70 75 80
Ser Gly Val Thr Arg Ile Ser Cys Gln Thr Leu Ile Val Lys Asn Glu
85 90 95
Asn Leu Glu Asn Leu Glu Glu Lys Glu Tyr Phe Gly Ile Val Ser Val
100 105 110
Arg Ile Leu Val His Glu Trp Pro Met Thr Ser Gly Ser Ser Leu Gln
115 120 125
Leu Ile Val Ile Gln Glu Glu Val Val Glu Ile Asp Gly Lys Gln Val
130 135 140
Gln Gln Lys Asp Val Thr Glu Ile Asp Ile Leu Val Lys Asn Arg Gly
145 150 155 160
Val Leu Arg His Ser Asn Tyr Thr Leu Pro Leu Glu Glu Ser Met Leu
165 170 175
Tyr Ser Ile Ser Arg Asp Ser Asp Ile Leu Phe Thr Leu Pro Asn Leu
180 185 190
Ser Lys Lys Glu Ser Val Ser Ser Leu Gln Thr Thr Ser Gln Tyr Leu
195 200 205
Ile Arg Asn Val Glu Thr Thr Val Asp Glu Asp Val Leu Pro Gly Lys
210 215 220
Leu Pro Glu Thr Pro Leu Arg Ala Glu Pro Pro Ser Ser Tyr Lys Val
225 230 235 240
Met Cys Gln Trp Met Glu Lys Phe Arg Lys Asp Leu Cys Arg Phe Trp
245 250 255

Ser Asn Val Phe Pro Val Phe Phe Gln Phe Leu Asn Ile Met Val Val
260 265 270
Gly Ile Thr Gly Ala Ala Val Val Ile Thr Ile Leu Lys Val Phe Phe
275 280 285
Pro Val Ser Glu Tyr Lys Gly Ile Leu Gln Leu Asp Lys Val Asp Val
290 295 300
Ile Pro Val Thr Ala Ile Asn Leu Tyr Pro Asp Gly Pro Glu Lys Arg
305 310 315 320
Ala Glu Asn Leu Glu Asp Lys Thr Cys Ile
325 330

Sequence No.: 23
Sequence length: 108
Sequence type: Amino acid
Topology: Linear
Sequence kind: Protein
Hypothetical: No
Original source:
Organism species: *Homo sapiens*
Cell kind: Osterosarcoma
Cell line: HU-2 OS
Clone name: HP10305
Sequence description

Met Ser Leu Thr Ser Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala
1 5 10 15
Val Thr Ile Ala Ala Gly Thr Ala Ala Ile Gly Tyr Leu Ala Tyr Lys
20 25 30
Arg Phe Tyr Val Lys Asp His Arg Asn Lys Ala Met Ile Asn Leu His
35 40 45
Ile Gln Lys Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp
50 55 60
Leu Gly Asp Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe
65 70 75 80
Pro Phe Cys Asp Gly Ala His Thr Lys His Asn Glu Glu Thr Gly Asp
85 90 95
Asn Val Gly Pro Leu Ile Ile Lys Lys Lys Glu Thr
100 105

Sequence No.: 24
Sequence length: 101
Sequence type: Amino acid

Topology: Linear
Sequence kind: Protein
Hypothetical: No
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Osterosarcoma
  Cell line: U-2 OS
  Clone name: HP10306
Sequence description

```
Met Asn Leu Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg
 1               5                  10                  15
Lys Tyr Tyr Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val
            20                  25                  30
Asn Ile Phe Trp Phe Phe Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr
        35                  40                  45
Glu Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe
    50                  55                  60
Leu Phe Trp Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile
65                  70                  75                  80
Tyr Arg Pro Arg Trp Gly Ala Leu Gly Asp Tyr Leu Ser Phe Thr Ile
                85                  90                  95
Pro Leu Gly Thr Pro
            100
```

Sequence No.: 25
Sequence length: 372
Sequence type: Amino acid
Topology: Linear
Sequence kind: Protein
Hypothetical: No
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Epidermoid carcinoma
  Cell line: KB
  Clone name: HP10328
Sequence description

```
Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala
 1               5                  10                  15
Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro
            20                  25                  30
Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala
```

35 40 45
Trp Pro Thr Pro Pro Thr Arg Pro Ala Pro Ala Pro Cys His Ala Asn
50 55 60
Thr Ser Met Val Thr His Pro Asp Phe Ala Thr Gln Pro Gln His Val
65 70 75 80
Gln Asn Phe Leu Leu Tyr Arg His Cys Arg His Phe Pro Leu Leu Gln
85 90 95
Asp Val Pro Pro Ser Lys Cys Ala Gln Pro Val Phe Leu Leu Leu Val
100 105 110
Ile Lys Ser Ser Pro Ser Asn Tyr Val Arg Arg Glu Leu Leu Arg Arg
115 120 125
Thr Trp Gly Arg Glu Arg Lys Val Arg Gly Leu Gln Leu Arg Leu Leu
130 135 140
Phe Leu Val Gly Thr Ala Ser Asn Pro His Glu Ala Arg Lys Val Asn
145 150 155 160
Arg Leu Leu Glu Leu Glu Ala Gln Thr His Gly Asp Ile Leu Gln Trp
165 170 175
Asp Phe His Asp Ser Phe Phe Asn Leu Thr Leu Lys Gln Val Leu Phe
180 185 190
Leu Gln Trp Gln Glu Thr Arg Cys Ala Asn Ala Ser Phe Val Leu Asn
195 200 205
Gly Asp Asp Asp Val Phe Ala His Thr Asp Asn Met Val Phe Tyr Leu
210 215 220
Gln Asp His Asp Pro Gly Arg His Leu Phe Val Gly Gln Leu Ile Gln
225 230 235 240
Asn Val Gly Pro Ile Arg Ala Phe Trp Ser Lys Tyr Tyr Val Pro Glu
245 250 255
Val Val Thr Gln Asn Glu Arg Tyr Pro Pro Tyr Cys Gly Gly Gly Gly
260 265 270
Phe Leu Leu Ser Arg Phe Thr Ala Ala Ala Leu Arg Arg Ala Ala His
275 280 285
Val Leu Asp Ile Phe Pro Ile Asp Asp Val Phe Leu Gly Met Cys Leu
290 295 300
Glu Leu Glu Gly Leu Lys Pro Ala Ser His Ser Gly Ile Arg Thr Ser
305 310 315 320
Gly Val Arg Ala Pro Ser Gln His Leu Ser Ser Phe Asp Pro Cys Phe
325 330 335
Tyr Arg Asp Leu Leu Leu Val His Arg Phe Leu Pro Tyr Glu Met Leu
340 345 350
Leu Met Trp Asp Ala Leu Asn Gln Pro Asn Leu Thr Cys Gly Asn Gln
355 360 365
Thr Gln Ile Tyr
370

Sequence No.: 26
Sequence length: 615
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Fibrosarcoma
  Cell line: HT-1080
  Clone name: HP00442
Sequence description

```
ATGACGGGGC TAGCACTGCT CTACTCCGGG GTCTTCGTGG CCTTCTGGGC CTGCGCGCTG    60
GCCGTGGGAG TCTGCTACAC CATTTTTGAT TTGGGCTTCC GCTTTGATGT GGCATGGTTC   120
CTGACGGAGA CTTCGCCCTT CATGTGGTCC AACCTGGGCA TTGGCCTAGC TATCTCCCTG   180
TCTGTGGTTG GGGCAGCCTG GGGCATCTAT ATTACCGGCT CCTCCATCAT TGGTGGAGGA   240
GTGAAGGCCC CCAGGATCAA GACCAAGAAC CTGGTCAGCA TCATCTTCTG TGAGGCTGTG   300
GCCATCTACG GCATCATCAT GGCAATTGTC ATTAGCAACA TGGCTGAGCC TTTCAGTGCC   360
ACAGACCCCA AGGCCATCGG CCATCGGAAC TACCATGCAG GCTACTCCAT GTTTGGGGCT   420
GGCCTCACCG TAGGCCTGTC TAACCTCTTC TGTGGAGTCT GCGTGGGCAT CGTGGGCAGT   480
GGGGCTGCCC TGGCCGATGC TCAGAACCCC AGCCTCTTTG TAAAGATTCT CATCGTGGAG   540
ATCTTTGGCA GCGCCATTGG CCTCTTTGGG GTCATCGTCG CAATTCTTCA GACCTCCAGA   600
GTGAAGATGG GTGAC                                                    615
```

Sequence No.: 27
Sequence length: 1113
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Leukocyte
  Clone name: HP00804
Sequence description

```
ATGTCCCATG AAAAGAGTTT TTTGGTGTCT GGGGACAACT ATCCTCCCCC CAACCCTGGA    60
TATCCGGGGG GGCCCCAGCC ACCCATGCCC CCCTATGCTC AGCCTCCCTA CCCTGGGGCC   120
CCTTACCCAC AGCCCCCTTT CCAGCCCTCC CCCTACGGTC AGCCAGGGTA CCCCCATGGC   180
CCCAGCCCCT ACCCCCAAGG GGGCTACCCA CAGGGTCCCT ACCCCCAAGG GGGCTACCCA   240
CAGGGCCCCT ACCCACAAGA GGGCTACCCA CAGGGCCCCT ACCCCCAAGG GGGCTACCCC   300
```

CAGGGGCCAT ATCCCCAGAG CCCCTTCCCC CCCAACCCCT ATGGACAGCC ACAGGTCTTC 360
CCAGGACAAG ACCCTGACTC ACCCCAGCAT GGAAACTACC AGGAGGAGGG TCCCCCATCC 420
TACTATGACA ACCAGGACTT CCCTGCCACC AACTGGGATG ACAAGAGCAT CCGACAGGCC 480
TTCATCCGCA AGGTGTTCCT AGTGCTGACC TTGCAGCTGT CGGTGACCCT GTCCACGGTG 540
TCTGTGTTCA CTTTTGTTGC GGAGGTGAAG GGCTTTGTCC GGGAGAATGT CTGGACCTAC 600
TATGTCTCCT ATGCTGTCTT CTTCATCTCT CTCATCGTCC TCAGCTGTTG TGGGGACTTC 660
CGGCGAAAGC ACCCCTGGAA CCTTGTTGCA CTGTCGGTCC TGACCGCCAG CCTGTCGTAC 720
ATGGTGGGGA TGATCGCCAG CTTCTACAAC ACCGAGGCAG TCATCATGGC CGTGGGCATC 780
ACCACAGCCG TCTGCTTCAC CGTCGTCATC TTCTCCATGC AGACCCGCTA CGACTTCACC 840
TCATGCATGG GCGTGCTCCT GGTGAGCATG GTGGTGCTCT TCATCTTCGC CATTCTCTGC 900
ATCTTCATCC GGAACCGCAT CCTGGAGATC GTGTACGCCT CACTGGGCGC TCTGCTCTTC 960
ACCTGCTTCC TCGCAGTGGA CACCCAGCTG CTGCTGGGGA ACAAGCAGCT GTCCCTGAGC 1020
CCAGAAGAGT ATGTGTTTGC TGCGCTGAAC CTGTACACAG ACATCATCAA CATCTTCCTG 1080
TACATCCTCA CCATCATTGG CCGCGCCAAG GAG 1113

Sequence No.: 28
Sequence length: 537
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Stomach cancer
  Clone name: HP01098
Sequence description

ATGCTGTCTC TAGACTTTTT GGACGATGTG CGGCGGATGA ACAAGCGGCA GCTCTATTAT 60
CAAGTCCTAA ATTTTGGAAT GATTGTCTCA TCGGCACTAA TGATCTGGAA GGGGTTAATG 120
GTAATAACTG GAAGTGAAAG TCCGATTGTA GTGGTGCTCA GTGGCAGCAT GGAACCTGCA 180
TTTCATAGAG GAGATCTTCT CTTTCTAACA AATCGAGTTG AAGATCCCAT ACGAGTGGGA 240
GAAATTGTTG TTTTTAGGAT AGAAGGAAGA GAGATTCCTA TAGTTCACCG AGTCTTGAAG 300
ATTCATGAAA AGCAAAATGG GCATATCAAG TTTTTGACCA AAGGAGATAA TAATGCGGTT 360
GATGACCGAG GCCTCTATAA ACAAGGACAA CATTGGCTAG AGAAAAAAGA TGTTGTGGGG 420
AGAGCCAGGG GATTTGTTCC TTATATTGGA ATTGTGACGA TCCTCATGAA TGACTATCCT 480
AAATTTAAGT ATGCAGTTCT CTTTTTGCTG GGTTTATTCG TGCTGGTTCA TCGTGAG 537

Sequence No.: 29
Sequence length: 1041
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear

Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Liver
  Clone name: HP01148
Sequence description

```
ATGGCTCTGC TATTCTCCTT GATCCTTGCC ATTTGCACCA GACCTGGATT CCTAGCGTCT     60
CCATCTGGAG TGCGGCTGGT GGGGGGCCTC CACCGCTGTG AAGGGCGGGT GGAGGTGGAA    120
CAGAAAGGCC AGTGGGGCAC CGTGTGTGAT GACGGCTGGG ACATTAAGGA CGTGGCTGTG    180
TTGTGCCGGG AGCTGGGCTG TGGAGCTGCC AGCGGAACCC CTAGTGGTAT TTTGTATGAG    240
CCACCAGCAG AAAAAGAGCA AAAGGTCCTC ATCCAATCAG TCAGTTGCAC AGGAACAGAA    300
GATACATTGG CTCAGTGTGA GCAAGAAGAA GTTTATGATT GTTCACATGA AGAAGATGCT    360
GGGGCATCGT GTGAGAACCC AGAGAGCTCT TTCTCCCCAG TCCCAGAGGG TGTCAGGCTG    420
GCTGACGGCC CTGGGCATTG CAAGGGACGC GTGGAAGTGA AGCACCAGAA CCAGTGGTAT    480
ACCGTGTGCC AGACAGGCTG GAGCCTCCGG GCCGCAAAGG TGGTGTGCCG GCAGCTGGGA    540
TGTGGGAGGG CTGTACTGAC TCAAAAACGC TGCAACAAGC ATGCCTATGG CCGAAAACCC    600
ATCTGGCTGA GCCAGATGTC ATGCTCAGGA CGAGAAGCAA CCCTTCAGGA TTGCCCTTCT    660
GGGCCTTGGG GGAAGAACAC CTGCAACCAT GATGAAGACA CGTGGGTCGA ATGTGAAGAT    720
CCCTTTGACT TGAGACTAGT AGGAGGAGAC AACCTCTGCT CTGGGCGACT GGAGGTGCTG    780
CACAAGGGCG TATGGGGCTC TGTCTGTGAT GACAACTGGG GAGAAAAGGA GGACCAGGTG    840
GTATGCAAGC AACTGGGCTG TGGGAAGTCC CTCTCTCCCT CCTTCAGAGA CCGGAAATGC    900
TATGGCCCTG GGGTTGGCCG CATCTGGCTG GATAATGTTC GTTGCTCAGG GGAGGAGCAG    960
TCCCTGGAGC AGTGCCAGCA CAGATTTTGG GGGTTTCACG ACTGCACCCA CCAGGAAGAT   1020
GTGGCTGTCA TCTGCTCAGG A                                             1041
```

Sequence No.: 30
Sequence length: 1662
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Liver
  Clone name: HP01293
Sequence description

```
ATGCCCACCG TGGATGACAT TCTGGAGCAG GTTGGGGAGT CTGGCTGGTT CCAGAAGCAA     60
GCCTTCCTCA TCTTATGCCT GCTGTCGGCT GCCTTTGCGC CCATCTGTGT GGGCATCGTC    120
TTCCTGGGTT TCACACCTGA CCACCACTGC CAGAGTCCTG GGGTGGCTGA GCTGAGCCAG    180
CGCTGTGGCT GGAGCCCTGC GGAGGAGCTG AACTATACAG TGCCAGGCCT GGGGCCCGCG    240
GGCGAGGCCT TCCTTGGCCA GTGCAGGCGC TATGAAGTGG ACTGGAACCA GAGCGCCCTC    300
```

AGCTGTGTAG ACCCCCTGGC TAGCCTGGCC ACCAACAGGA GCCACCTGCC GCTGGGTCCC 360
TGCCAGGATG GCTGGGTGTA TGACACGCCC GGCTCTTCCA TCGTCACTGA GTTCAACCTG 420
GTGTGTGCTG ACTCCTGGAA GCTGGACCTC TTTCAGTCCT GTTTGAATGC GGGCTTCTTC 480
TTTGGCTCTC TCGGTGTTGG CTACTTTGCA GACAGGTTTG GCCGTAAGCT GTGTCTCCTG 540
GGAACTGTGC TGGTCAACGC GGTGTCGGGC GTGCTCATGG CCTTCTCGCC CAACTACATG 600
TCCATGCTGC TCTTCCGCCT GCTGCAGGGC CTGGTCAGCA AGGGCAACTG GATGGCTGGC 660
TACACCCTAA TCACAGAATT TGTTGGCTCG GGCTCCAGAA GAACGGTGGC GATCATGTAC 720
CAGATGGCCT TCACGGTGGG GCTGGTGGCG CTTACCGGGC TGGCCTACGC CCTGCCTCAC 780
TGGCGCTGGC TGCAGCTGGC AGTCTCCCTG CCCACCTTCC TCTTCCTGCT CTACTACTGG 840
TGTGTGCCGG AGTCCCCTCG GTGGCTGTTA TCACAAAAAA GAAACACTGA AGCAATAAAG 900
ATAATGGACC ACATCGCTCA AAAGAATGGG AAGTTGCCTC CTGCTGATTT AAAGATGCTT 960
TCCCTCGAAG AGGATGTCAC CGAAAAGCTG AGCCCTTCAT TTGCAGACCT GTTCCGCACG 1020
CCGCGCCTGA GGAAGCGCAC CTTCATCCTG ATGTACCTGT GGTTCACGGA CTCTGTGCTC 1080
TATCAGGGGC TCATCCTGCA CATGGGCGCC ACCAGCGGGA ACCTCTACCT GGATTTCCTT 1140
TACTCCGCTC TGGTCGAAAT CCCGGGGGCC TTCATAGCCC TCATCACCAT TGACCGCGTG 1200
GGCCGCATCT ACCCCATGGC CGTGTCAAAT TTGTTGGCGG GGGCAGCCTG CCTCGTCATG 1260
ATTTTTATCT CACCTGACCT GCACTGGTTA AACATCATAA TCATGTGTGT TGGCCGAATG 1320
GGAATCACCA TTGCAATACA AATGATCTGC CTGGTGAATG CTGAGCTGTA CCCCACATTC 1380
GTCAGGAACC TCGGAGTGAT GGTGTGTTCC TCCCTGTGTG ACATAGGTGG GATAATCACC 1440
CCCTTCATAG TCTTCAGGCT GAGGGAGGTC TGGCAAGCCT TGCCCCTCAT TTTGTTTGCG 1500
GTGTTGGGCC TGCTTGCCGC GGGAGTGACG CTACTTCTTC CAGAGACCAA GGGGGTCGCT 1560
TTGCCAGAGA CCATGAAGGA CGCCGAGAAC CTTGGGAGAA AAGCAAAGCC CAAAGAAAAC 1620
ACGATTTACC TTAAGGTCCA AACCTCAGAA CCCTCGGGCA CC 1662

Sequence No.: 31
Sequence length: 1050
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Epidermoid carcinoma
  Cell line: KB
  Clone name: HP10013
Sequence description

ATGGCTGTGT TTGTCGTGCT CCTGGCGTTG GTGGCGGGTG TTTTGGGGAA CGAGTTTAGT 60
ATATTAAAAT CACCAGGGTC TGTTGTTTTC CGAAATGGAA ATTGGCCTAT ACCAGGAGAG 120
CGGATCCCAG ACGTGGCTGC ATTGTCCATG GGCTTCTCTG TGAAAGAAGA CCTTTCTTGG 180
CCAGGACTCG CAGTGGGTAA CCTGTTTCAT CGTCCTCGGG CTACCGTCAT GGTGATGGTG 240
AAGGGAGTGA ACAAACTGGC TCTACCCCCA GGCAGTGTCA TTTCGTACCC TTTGGAGAAT 300
GCAGTTCCTT TTAGTCTTGA CAGTGTTGCA AATTCCATTC ACTCCTTATT TTCTGAGGAA 360

ACTCCTGTTG TTTTGCAGTT GGCTCCCAGT GAGGAAAGAG TGTATATGGT AGGGAAGGCA 420
AACTCAGTGT TTGAAGACCT TTCAGTCACC TTGCGCCAGC TCCGTAATCG CCTGTTTCAA 480
GAAAACTCTG TTCTCAGTTC ACTCCCCCTC AATTCTCTGA GTAGGAACAA TGAAGTTGAC 540
CTGCTCTTTC TTTCTGAACT GCAAGTGCTA CATGATATTT CAAGCTTGCT GTCTCGTCAT 600
AAGCATCTAG CCAAGGATCA TTCTCCTGAT TTATATTCAC TGGAGCTGGC AGGTTTGGAT 660
GAAATTGGGA AGCGTTATGG GGAAGACTCT GAACAATTCA GAGATGCTTC TAAGATCCTT 720
GTTGACGCTC TGCAAAAGTT TGCAGATGAC ATGTACAGTC TTTATGGTGG GAATGCAGTG 780
GTAGAGTTAG TCACTGTCAA GTCATTTGAC ACCTCCCTCA TTAGGAAGAC AAGGACTATC 840
CTTGAGGCAA AACAAGCGAA GAACCCAGCA AGTCCCTATA ACCTTGCATA TAAGTATAAT 900
TTTGAATATT CCGTGGTTTT CAACATGGTA CTTTGGATAA TGATCGCCTT GGCCTTGGCT 960
GTGATTATCA CCTCTTACAA TATTTGGAAC ATGGATCCTG GATATGATAG CATCATTTAT 1020
AGGATGACAA ACCAGAAGAT TCGAATGGAT 1050

Sequence No.: 32
Sequence length: 627
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Fibrosarcoma
  Cell line: HT-1080
  Clone name: HP10034
Sequence description

ATGGTGTCCT CTCCCTGCAC GCAGGCAAGC TCACGGACTT GCTCCCGTAT CCTGGGACTG 60
AGCCTTGGGA CTGCAGCCCT GTTTGCTGCT GGGGCCAACG TGGCACTCCT CCTTCCTAAC 120
TGGGATGTCA CCTACCTGTT GAGGGGCCTC CTTGGCAGGC ATGCCATGCT GGGAACTGGG 180
CTCTGGGGAG GAGGCCTCAT GGTACTCACT GCAGCTATCC TCATCTCCTT GATGGGCTGG 240
AGATACGGCT GCTTCAGTAA GAGTGGGCTC TGTCGAAGCG TGCTTACTGC TCTGTTGTCA 300
GGTGGCCTGG CTTTACTTGG AGCCCTGATT TGCTTTGTCA CTTCTGGAGT TGCTCTGAAA 360
GATGGTCCTT TTTGCATGTT TGATGTTTCA TCCTTCAATC AGACACAAGC TTGGAAATAT 420
GGTTACCCAT TCAAAGACCT GCATAGTAGG AATTATCTGT ATGACCGTTC GCTCTGGAAC 480
TCCGTCTGCC TGGAGCCCTC TGCAGCTGTT GTCTGGCACG TGTCCCTCTT CTCCGCCCTT 540
CTGTGCATCA GCCTGCTCCA GCTTCTCCTG GTGGTCGTTC ATGTCATCAA CAGCCTCCTG 600
GGCCTTTTCT GCAGCCTCTG CGAGAAG 627

Sequence No.: 33
Sequence length: 489
Sequence type: Nucleic acid
Strandedness: Double

Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Fibrosarcoma
  Cell line: HT-1080
  Clone name: HP10050
Sequence description

```
ATGGCGGCTG GGCTGTTTGG TTTGAGCGCT CGCCGTCTTT TGGCGGCAGC GGCGACGCGA    60
GGGCTCCCGG CCGCCCGCGT CCGCTGGGAA TCTAGCTTCT CCAGGACTGT GGTCGCCCCG   120
TCCGCTGTGG CGGGAAAGCG GCCCCCAGAA CCGACCACAC CGTGGCAAGA GGACCCAGAA   180
CCCGAGGACG AAAACTTGTA TGAGAAGAAC CCAGACTCCC ATGGTTATGA CAAGGACCCC   240
GTTTTGGACG TCTGGAACAT GCGACTTGTC TTCTTCTTTG GCGTCTCCAT CATCCTGGTC   300
CTTGGCAGCA CCTTTGTGGC CTATCTGCCT GACTACAGGT GCACAGGGTG TCCAAGAGCG   360
TGGGATGGGA TGAAAGAGTG GTCCCGCCGC GAAGCTGAGA GGCTTGTGAA ATACCGAGAG   420
GCCAATGGCC TTCCCATCAT GGAATCCAAC TGCTTCGACC CCAGCAAGAT CCAGCTGCCA   480
GAGGATGAG                                                           489
```

Sequence No.: 34
Sequence length: 276
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Stomach cancer
  Clone name: HP10071
Sequence description

```
ATGACGAAAT TAGCGCAGTG GCTTTGGGGA CTAGCGATCC TGGGCTCCAC CTGGGTGGCC    60
CTGACCACGG GAGCCTTGGG CCTGGAGCTG CCCTTGTCCT GCCAGGAAGT CCTGTGGCCA   120
CTGCCCGCCT ACTTGCTGGT GTCCGCCGGC TGCTATGCCC TGGGCACTGT GGGCTATCGT   180
GTGGCCACTT TTCATGACTG CGAGGACGCC GCACGCGAGC TGCAGAGCCA GATACAGGAG   240
GCCCGAGCCG ACTTAGCCCG CAGGGGGCTG CGCTTC                             276
```

Sequence No.: 35
Sequence length: 516
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear

Sequence kind: cDNA to mRNA
Original source:
Organism species: *Homo sapiens*
Cell kind: Lymphoma
Cell line: U937
Clone name: HP10076
Sequence description

```
ATGGAATATT TGGCTCATCC CAGTACACTC GGCTTGGCTG TTGGAGTTGC TTGTGGCATG      60
TGCCTGGGCT GGAGCCTTCG AGTATGCTTT GGGATGCTCC CCAAAAGCAA GACGAGCAAG     120
ACACACACAG ATACTGAAAG TGAAGCAAGC ATCTTGGGAG ACAGCGGGGA GTACAAGATG     180
ATTCTTGTGG TTCGAAATGA CTTAAAGATG GGAAAAGGGA AAGTGGCTGC CCAGTGCTCT     240
CATGCTGCTG TTTCAGCCTA CAAGCAGATT CAAAGAAGAA ATCCTGAAAT GCTCAAACAA     300
TGGGAATACT GTGGCCAGCC CAAGGTGGTG GTCAAAGCTC CTGATGAAGA AACCCTGATT     360
GCATTATTGG CCCATGCAAA AATGCTGGGA CTGACTGTAA GTTTAATTCA AGATGCTGGA     420
CGTACTCAGA TTGCACCAGG CTCTCAAACT GTCCTAGGGA TTGGGCCAGG ACCAGCAGAC     480
CTAATTGACA AAGTCACTGG TCACCTAAAA CTTTAC                               516
```

Sequence No.: 36
Sequence length: 447
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
Organism species: *Homo sapiens*
Cell kind: Lymphoma
Cell line: U937
Clone name: HP10085
Sequence description

```
ATGATGACCA AACATAAAAA GTGTTTTATA ATTGTTGGTG TTTTAATAAC AACTAATATT      60
ATTACTCTGA TAGTTAAACT AACTCGAGAT TCTCAGAGTT TATGCCCCTA TGATTGGATT     120
GGTTTCCAAA ACAAATGCTA TTATTTCTCT AAAGAAGAAG GAGATTGGAA TTCAAGTAAA     180
TACAACTGTT CCACTCAACA TGCCGACCTA ACTATAATTG ACAACATAGA AGAAATGAAT     240
TTTCTTAGGC GGTATAAATG CAGTTCTGAT CACTGGATTG GACTGAAGAT GGCAAAAAAT     300
CGAACAGGAC AATGGGTAGA TGGAGCTACA TTTACCAAAT CGTTTGGCAT GAGAGGGAGT     360
GAAGGATGTG CCTACCTCAG CGATGATGGT GCAGCAACAG CTAGATGTTA CACCGAAAGA     420
AAATGGATTT GCAGGAAAAG AATACAC                                         447
```

Sequence No.: 37
Sequence length: 564

Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Stonach cancer
  Clone name: HP10122
Sequence description

```
ATGAGCACTA TGTTCGCGGA CACTCTCCTC ATCGTTTTTA TCTCTGTGTG CACGGCTCTG    60
CTCGCAGAGG GCATAACCTG GGTCCTGGTT TACAGGACAG ACAAGTACAA GAGACTGAAG   120
GCAGAAGTGG AAAAACAGAG TAAAAAATTG GAAAAGAAGA AGGAAACAAT AACAGAGTCA   180
GCTGGTCGAC AACAGAAAAA GAAAATAGAG AGACAAGAAG AGAAACTGAA GAATAACAAC   240
AGAGATCTAT CAATGGTTCG AATGAAATCC ATGTTTGCTA TTGGCTTTTG TTTTACTGCC   300
CTAATGGGAA TGTTCAATTC CATATTTGAT GGTAGAGTGG TGGCAAAGCT TCCTTTTACC   360
CCTCTTTCTT ACATCCAAGG ACTGTCTCAT CGAAATCTGC TGGGAGATGA CACCACAGAC   420
TGTTCCTTCA TTTTCCTGTA TATTCTCTGT ACTATGTCGA TTCGACAGAA CATTCAGAAG   480
ATTCTCGGCC TTGCCCCTTC ACGAGCCGCC ACCAAGCAGG CAGGTGGATT TCTTGGCCCA   540
CCACCTCCTT CTGGGAAGTT CTCT                                           564
```

Sequence No.: 38
Sequence length: 645
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Lymphoma
  Cell line: U937
  Clone name: HP10136
Sequence description

```
ATGGTGTTGC TAACAATGAT CGCCCGAGTG GCGGACGGGC TCCCGCTGGC CGCCTCGATG    60
CAGGAGGACG AACAGTCTGG CCGGGACCTT CAACAGTATC AGAGTCAGGC TAAGCAACTC   120
TTTCGAAAGT TGAATGAACA GTCCCCTACC AGATGTACCT TGGAAGCAGG AGCCATGACT   180
TTTCACTACA TTATTGAGCA GGGGGTGTGT TATTTGGTTT TATGTGAAGC TGCCTTCCCT   240
AAGAAGTTGG CTTTTGCCTA CCTAGAAGAT TTGCACTCAG AATTTGATGA ACAGCATGGA   300
AAGAAGGTGC CCACTGTGTC CCGACCCTAT TCCTTTATTG AATTTGATAC TTTCATTCAG   360
AAAACCAAGA AGCTCTACAT TGACAGTCGT GCTCGAAGAA ATCTAGGCTC CATCAACACT   420
GAATTGCAAG ATGTGCAGAG GATCATGGTG GCCAATATTG AAGAAGTGTT ACAACGAGGA   480
GAAGCACTCT CAGCATTGGA TTCAAAGGCT AACAATTTGT CCAGTCTGTC CAAGAAATAC   540
```

CGCCAGGATG CGAAGTACTT GAACATGCGT TCCACTTATG CCAAACTTGC AGCAGTAGCT 600
GTATTTTTCA TCATGTTAAT AGTGTATGTC CGATTCTGGT GGCTG 645

Sequence No.: 39
Sequence length: 336
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
Organism species: *Homo sapiens*
Cell kind: Stomach cancer
Clone name: HP10175
Sequence description

ATGCAGGACA CTGGCTCAGT AGTGCCTTTG CATTGGTTTG GCTTTGGCTA CGCAGCACTG 60
GTTGCTTCTG GTGGGATCAT TGGCTATGTA AAAGCAGGCA GCGTGCCGTC CCTGGCTGCA 120
GGGCTGCTCT TTGGCAGTCT AGCCGGCCTG GGTGCTTACC AGCTGTCTCA GGATCCAAGG 180
AACGTTTGGG TTTTCCTAGC TACATCTGGT ACCTTGGCTG GCATTATGGG AATGAGGTTC 240
TACCACTCTG GAAAATTCAT GCCTGCAGGT TTAATTGCAG GTGCCAGTTT GCTGATGGTC 300
GCCAAAGTTG GAGTTAGTAT GTTCAACAGA CCCCAT 336

Sequence No.: 40
Sequence length: 342
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
Organism species: *Homo sapiens*
Cell kind: Epidermoid carcinoma
Cell line: KB
Clone name: HP10179
Sequence description

ATGGAGAAGC CCCTCTTCCC ATTAGTGCCT TTGCATTGGT TTGGCTTTGG CTACACAGCA 60
CTGGTTGTTT CTGGTGGGAT CGTTGGCTAT GTAAAAACAG GCAGCGTGCC GTCCCTGGCT 120
GCAGGGCTGC TCTTCGGCAG TCTAGCCGGC CTGGGTGCTT ACCAGCTGTA TCAGGATCCA 180
AGGAACGTTT GGGGTTTCCT AGCCGCTACA TCTGTTACTT TTGTTGGTGT TATGGGAATG 240
AGATCCTACT ACTATGGAAA ATTCATGCCT GTAGGTTTAA TTGCAGGTGC CAGTTTGCTG 300
ATGGCCGCCA AAGTTGGAGT TCGTATGTTG ATGACATCTG AT 342

Sequence No.: 41
Sequence length: 981
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Fibrosarcoma
  Cell line: HT-1080
  Clone name: HP10196
Sequence description

```
ATGGCGGCGG CGGCGGCGGC GGCTGCAGCT ACGAACGGGA CCGGAGGAAG CAGCGGGATG     60
GAGGTGGATG CAGCAGTAGT CCCCAGCGTG ATGGCCTGCG GAGTGACTGG GAGTGTTTCC    120
GTCGCTCTCC ATCCCCTTGT CATTCTCAAC ATCTCAGACC ACTGGATCCG CATGCGCTCC    180
CAGGAGGGGC GGCCTGTGCA GGTGATTGGG GCTCTGATTG GCAAGCAGGA GGGCCGAAAT    240
ATCGAGGTGA TGAACTCCTT TGAGCTGCTG TCCCACACCG TGGAAGAGAA GATTATCATT    300
GACAAGGAAT ATTATTACAC CAAGGAGGAG CAGTTTAAAC AGGTGTTCAA GGAGCTGGAG    360
TTTCTGGGTT GGTATACCAC AGGGGGGCCA CCTGACCCCT CGGACATCCA CGTCCATAAG    420
CAGGTGTGTG AGATCATCGA GAGCCCCCTC TTTCTGAAGT TGAACCCTAT GACCAAGCAC    480
ACAGATCTTC CTGTCAGCGT TTTTGAGTCT GTCATTGATA TAATCAATGG AGAGGCCACA    540
ATGCTGTTTG CTGAGCTGAC CTACACTCTG GCCACAGAGG AAGCGGAACG CATTGGTGTA    600
GACCACGTAG CCCGAATGAC AGCAACAGGC AGTGGAGAGA ACTCCACTGT GGCTGAACAC    660
CTGATAGCAC AGCACAGCGC CATCAAGATG CTGCACAGCC GCGTCAAGCT CATCTTGGAG    720
TACGTCAAGG CCTCTGAAGC GGGAGAGGTC CCCTTTAATC ATGAGATCCT GCGGGAGGCC    780
TATGCTCTGT GTCACTGTCT CCCGGTGCTC AGCACAGACA AGTTCAAGAC AGATTTTTAT    840
GATCAATGCA ACGACGTGGG GCTCATGGCC TACCTCGGCA CCATCACCAA AACGTGCAAC    900
ACCATGAACC AGTTTGTGAA CAAGTTCAAT GTCCTCTACG ACCGACAAGG CATCGGCAGG    960
AGAATGCGCG GGCTCTTTTT C                                              981
```

Sequence No.: 42
Sequence length: 1119
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Fibrosarcoma
  Cell line: HT-1080
  Clone name: HP10235
Sequence description

ATGACCCTAT GTGCCATGCT GCCCCTGCTG TTATTCACCT ACCTCAACTC CTTCCTGCAT 60
CAGAGGATCC CCCAGTCCGT ACGGATCCTG GGCAGCCTGG TGGCCATCCT GCTGGTGTTT 120
CTGATCACTG CCATCCTGGT GAAGGTGCAG CTGGATGCTC TGCCCTTCTT TGTCATCACC 180
ATGATCAAGA TCGTGCTCAT TAATTCATTT GGTGCCATCC TGCAGGGCAG CCTGTTTGGT 240
CTGGCTGGCC TTCTGCCTGC CAGCTACACG GCCCCCATCA TGAGTGGCCA GGGCCTAGCA 300
GGCTTCTTTG CCTCCGTGGC CATGATCTGC GCTATTGCCA GTGGCTCGGA GCTATCAGAA 360
AGTGCCTTCG GCTACTTTAT CACAGCCTGT GCTGTTATCA TTTTGACCAT CATCTGTTAC 420
CTGGGCCTGC CCCGCCTGGA ATTCTACCGC TACTACCAGC AGCTCAAGCT TGAAGGACCC 480
GGGGAGCAGG AGACCAAGTT GGACCTCATT AGCAAAGGAG AGGAGCCAAG AGCAGGCAAA 540
GAGGAATCTG GAGTTTCAGT CTCCAACTCT CAGCCCACCA ATGAAAGCCA CTCTATCAAA 600
GCCATCCTGA AAAATATCTC AGTCCTGGCT TTCTCTGTCT GCTTCATCTT CACTATCACC 660
ATTGGGATGT TTCCAGCCGT GACTGTTGAG GTCAAGTCCA GCATCGCAGG CAGCAGCACC 720
TGGGAACGTT ACTTCATTCC TGTGTCCTGT TTCTTGACTT TCAATATCTT TGACTGGTTG 780
GGCCGGAGCC TCACAGCTGT ATTCATGTGG CCTGGGAAGG ACAGCCGCTG GCTGCCAAGC 840
CTGGTGCTGG CCCGGCTGGT GTTTGTGCCA CTGCTGCTGC TGTGCAACAT TAAGCCCCGC 900
CGCTACCTGA CTGTGGTCTT CGAGCACGAT GCCTGGTTCA TCTTCTTCAT GGCTGCCTTT 960
GCCTTCTCCA ACGGCTACCT CGCCAGCCTC TGCATGTGCT TCGGGCCCAA GAAAGTGAAG 1020
CCAGCTGAGG CAGAGACCGC AGGAGCCATC ATGGCCTTCT TCCTGTGTCT GGGTCTGGCA 1080
CTGGGGGCTG TTTTCTCCTT CCTGTTCCGG GCAATTGTG 1119

Sequence No.: 43
Sequence length: 549
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Stomach cancer
  Clone name: HP10297
Sequence description

ATGAAGCTCT TATCTTTGGT GGCTGTGGTC GGGTGTTTGC TGGTGCCCCC AGCTGAAGCC 60
AACAAGAGTT CTGAAGATAT CCGGTGCAAA TGCATCTGTC CACCTTATAG AAACATCAGT 120
GGGCACATTT ACAACCAGAA TGTATCCCAG AAGGACTGCA ACTGCCTGCA CGTGGTGGAG 180
CCCATGCCAG TGCCTGGCCA TGACGTGGAG GCCTACTGCC TGCTGTGCGA GTGCAGGTAC 240
GAGGAGCGCA GCACCACCAC CATCAAGGTC ATCATTGTCA TCTACCTGTC CGTGGTGGGT 300
GCCCTGTTGC TCTACATGGC CTTCCTGATG CTGGTGGACC CTCTGATCCG AAAGCCGGAT 360
GCATACACTG AGCAACTGCA CAATGAGGAG GAGAATGAGG ATGCTCGCTC TATGGCAGCA 420
GCTGCTGCAT CCCTCGGGGG ACCCCGAGCA AACACAGTCC TGGAGCGTGT GGAAGGTGCC 480
CAGCAGCGGT GGAAGCTGCA GGTGCAGGAG CAGCGGAAGA CAGTCTTCGA TCGGCACAAG 540
ATGCTCAGC 549

Sequence No.: 44
Sequence length: 348
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
 Organism species: *Homo sapiens*
 Cell kind: Stomach cancer
 Clone name: HP10299
Sequence description

```
ATGGCCAGTA CAGTGGTAGC AGTTGGACTG ACCATTGCTG CTGCAGGATT TGCAGGCCGT    60
TACGTTTTGC AAGCCATGAA GCATATGGAG CCTCAAGTAA AACAAGTTTT TCAAAGCCTA   120
CCAAAATCTG CCTTCAGTGG TGGCTATTAT AGAGGTGGGT TTGAACCCAA AATGACAAAA   180
CGGGAAGCA GCATTAATAC TAGGTGTAAG CCCTACTGCC AATAAAGGGA AAATAAGAGA    240
GCTCATCGAC GAATTATGCT TTTAAATCAT CCTGACAAAG GAGGATCTCC TTATATAGCA   300
GCCAAAATCA ATGAAGCTAA AGATTTACTA GAAGGTCAAG CTAAAAAA                348
```

Sequence No.: 45
Sequence length: 456
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
 Organism species: *Homo sapiens*
 Cell kind: Epidermoid carcinoma
 Cell line: KB
 Clone name: HP10301
Sequence description

```
ATGGCTGTCC TCTCTAAGGA ATATGGTTTT GTGCTTCTAA CTGGTGCTGC CAGCTTTATA    60
ATGGTGGCCC ACCTAGCCAT CAATGTTTCC AAGGCCCGCA AGAAGTACAA AGTGGAGTAT   120
CCTATCATGT ACAGCACGGA CCCTGAAAAT GGGCACATCT TCAACTGCAT TCAGCGAGCC   180
CACCAGAACA CGTTGGAAGT GTATCCTCCC TTCTTATTTT TTCTAGCTGT TGGAGGTGTT   240
TACCACCCGC GTATAGCTTC TGGCCTGGGC TTGGCCTGGA TTGTTGGACG AGTTCTTTAT   300
GCTTATGGCT ATTACACGGG AGAACCCAGC AAGCGTAGTC GAGGAGCCCT GGGGTCCATC   360
GCCCTCCTGG GCTTGGTGGG CACAACTGTG TGCTCTGCTT TCCAGCATCT TGGTTGGGTT   420
AAAAGTGGCT TGGGCAGTGG ACCCAAATGC TGCCAT                             456
```

Sequence No.: 46
Sequence length: 1677
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Liver
  Clone name: HP10302
Sequence description

```
ATGGCCCCCA CGCTGCAACA GGCGTACCGG AGGCGCTGGT GGATGGCCTG CACGGCTGTG     60
CTGGAGAACC TCTTCTTCTC TGCTGTACTC CTGGGCTGGG GCTCCCTGTT GATCATTCTG    120
AAGAACGAGG GCTTCTATTC CAGCACGTGC CCAGCTGAGA GCAGCACCAA CACCACCCAG    180
GATGAGCAGC GCAGGTGGCC AGGCTGTGAC CAGCAGGACG AGATGCTCAA CCTGGGCTTC    240
ACCATTGGTT CCTTCGTGCT CAGCGCCACC ACCCTGCCAC TGGGGATCCT CATGGACCGC    300
TTTGGCCCCC GACCCGTGCG GCTGGTTGGC AGTGCCTGCT TCACTGCGTC CTGCACCCTC    360
ATGGCCCTGG CCTCCCGGGA CGTGGAAGCT CTGTCTCCGT TGATATTCCT GGCGCTGTCC    420
CTGAATGGCT TTGGTGGCAT CTGCCTAACG TTCACTTCAC TCACGCTGCC CAACATGTTT    480
GGGAACCTGC GCTCCACGTT AATGGCCCTC ATGATTGGCT CTTACGCCTC TTCTGCCATT    540
ACGTTCCCAG GAATCAAGCT GATCTACGAT GCCGGTGTGG CCTTCGTGGT CATCATGTTC    600
ACCTGGTCTG GCCTGGCCTG CCTTATCTTT CTGAACTGCA CCCTCAACTG GCCCATCGAA    660
GCCTTTCCTG CCCCTGAGGA AGTCAATTAC ACGAAGAAGA TCAAGCTGAG TGGGCTGGCC    720
CTGGACCACA AGGTGACAGG TGACCTCTTC TACACCCATG TGACCACCAT GGGCCAGAGG    780
CTCAGCCAGA AGGCCCCCAG CCTGGAGGAC GGTTCGGATG CCTTCATGTC ACCCCAGGAT    840
GTTCGGGGCA CCTCAGAAAA CCTTCCTGAG AGGTCTGTCC CCTTACGCAA GAGCCTCTGC    900
TCCCCCACTT TCCTGTGGAG CCTCCTCACC ATGGGCATGA CCCAGCTGCG GATCATCTTC    960
TACATGGCTG CTGTGAACAA GATGCTGGAG TACCTTGTGA CTGGTGGCCA GGAGCATGAG   1020
ACAAATGAAC AGCAACAAAA GGTGGCAGAG ACAGTTGGGT TCTACTCCTC CGTCTTCGGG   1080
GCCATGCAGC TGTTGTGCCT TCTCACCTGC CCCCTCATTG GCTACATCAT GGACTGGCGG   1140
ATCAAGGACT GCGTGGACGC CCCAACTCAG GGCACTGTCC TCGGAGATGC CAGGGACGGG   1200
GTTGCTACCA AATCCATCAG ACCACGCTAC TGCAAGATCC AAAAGCTCAC CAATGCCATC   1260
AGTGCCTTCA CCCTGACCAA CCTGCTGCTT GTGGGTTTTG GCATCACCTG TCTCATCAAC   1320
AACTTACACC TCCAGTTTGT GACCTTTGTC CTGCACACCA TTGTTCGAGG TTTCTTCCAC   1380
TCAGCCTGTG GGAGTCTCTA TGCTGCAGTG TTCCCATCCA ACCACTTTGG GACGCTGACA   1440
GGCCTGCAGT CCCTCATCAG TGCTGTGTTC GCCTTGCTTC AGCAGCCACT TTTCATGGCG   1500
ATGGTGGGAC CCCTGAAAGG AGAGCCCTTC TGGGTGAATC TGGGCCTCCT GCTATTCTCA   1560
CTCCTGGGAT TCCTGTTGCC TTCCTACCTC TTCTATTACC GTGCCCGGCT CCAGCAGGAG   1620
TACGCCGCCA ATGGGATGGG CCCACTGAAG GTGCTTAGCG GCTCTGAGGT GACCGCA      1677
```

Sequence No.: 47
Sequence length: 990

Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Osterosarcoma
  Cell line: U-2 OS
  Clone name: HP10304
Sequence description

```
ATGGAGGGCG CTCCACCGGG GTCGCTCGCC CTCCGGCTCC TGCTGTTCGT GGCGCTACCC    60
GCCTCCGGCT GGCTGACGAC GGGCGCCCCC GAGCCGCCGC CGCTGTCCGG AGCCCCACAG   120
GACGGCATCA GAATTAATGT AACTACACTG AAAGATGATG GGGACATATC TAAACAGCAG   180
GTTGTTCTTA ACATAACCTA TGAGAGTGGA CAGGTGTATG TAAATGACTT ACCTGTAAAT   240
AGTGGTGTAA CCCGAATAAG CTGTCAGACT TTGATAGTGA AGAATGAAAA TCTTGAAAAT   300
TTGGAGGAAA AAGAATATTT TGGAATTGTC AGTGTAAGGA TTTTAGTTCA TGAGTGGCCT   360
ATGACATCTG GTTCCAGTTT GCAACTAATT GTCATTCAAG AAGAGGTAGT AGAGATTGAT   420
GGAAAACAAG TTCAGCAAAA GGATGTCACT GAAATTGATA TTTTAGTTAA GAACCGGGGA   480
GTACTCAGAC ATTCAAACTA TACCCTCCCT TTGGAAGAAA GCATGCTCTA CTCTATTTCT   540
CGAGACAGTG ACATTTTATT TACCCTTCCT AACCTCTCCA AAAAAGAAAG TGTTAGTTCA   600
CTGCAAACCA CTAGCCAGTA TCTTATCAGG AATGTGGAAA CCACTGTAGA TGAAGATGTT   660
TTACCTGGCA AGTTACCTGA AACTCCTCTC AGAGCAGAGC CGCCATCTTC ATATAAGGTA   720
ATGTGTCAGT GGATGGAAAA GTTTAGAAAA GATCTGTGTA GGTTCTGGAG CAACGTTTTC   780
CCAGTATTCT TTCAGTTTTT GAACATCATG GTGGTTGGAA TTACAGGAGC AGCTGTGGTA   840
ATAACCATCT TAAAGGTGTT TTTCCCAGTT TCTGAATACA AAGGAATTCT TCAGTTGGAT   900
AAAGTGGACG TCATACCTGT GACAGCTATC AACTTATATC CAGATGGTCC AGAGAAAAGA   960
GCTGAAAACC TTGAAGATAA AACATGTATT                                     990
```

Sequence No.: 48
Sequence length: 324
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Osterosarcoma
  Cell line: U-2 OS
  Clone name: HP10305
Sequence description

```
ATGAGTCTGA CTTCCAGTTC CAGCGTACGA GTTGAATGGA TCGCAGCAGT TACCATTGCT    60
```

GCTGGGACAG CTGCAATTGG TTATCTAGCT TACAAAAGAT TTTATGTTAA AGATCATCGA 120
AATAAAGCTA TGATAAACCT TCACATCCAG AAAGACAACC CCAAGATAGT ACATGCTTTT 180
GACATGGAGG ATTTGGGAGA TAAAGCTGTG TACTGCCGTT GTTGGAGGTC CAAAAAGTTC 240
CCATTCTGTG ATGGGGCTCA CACAAAACAT AACGAAGAGA CTGGAGACAA TGTGGGCCCT 300
CTGATCATCA AGAAAAAAGA AACT 324

Sequence No.: 49
Sequence length: 303
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Osterosarcoma
  Cell line: U-2 OS
  Clone name: HP10306
Sequence description

ATGAACCTGG AGCGAGTGTC CAATGAGGAG AAATTGAACC TGTGCCGGAA GTACTACCTG 60
GGGGGGTTTG CTTTCCTGCC TTTTCTCTGG TTGGTCAACA TCTTCTGGTT CTTCCGAGAG 120
GCCTTCCTTG TCCCAGCCTA CACAGAACAG AGCCAAATCA AAGGCTATGT CTGGCGCTCA 180
GCTGTGGGCT TCCTCTTCTG GGTGATAGTG CTCACCTCCT GGATCACCAT CTTCCAGATC 240
TACCGGCCCC GCTGGGGTGC CCTTGGGGAC TACCTCTCCT TCACCATACC CCTGGGCACC 300
CCC 303

Sequence No.: 50
Sequence length: 1116
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Epidermoid carcinoma
  Cell line: KB
  Clone name: HP10328
Sequence description

ATGAAGTATC TCCGGCACCG GCGGCCCAAT GCCACCCTCA TTCTGGCCAT CGGCGCTTTC 60
ACCCTCCTCC TCTTCAGTCT GCTAGTGTCA CCACCCACCT GCAAGGTCCA GGAGCAGCCA 120
CCGGCGATCC CCGAGGCCCT GGCCTGGCCC ACTCCACCCA CCCGCCCAGC CCCGGCCCCG 180

TGCCATGCCA ACACCTCTAT GGTCACCCAC CCGGACTTCG CCACGCAGCC GCAGCACGTT 240
CAGAACTTCC TCCTGTACAG ACACTGCCGC CACTTTCCCC TGCTGCAGGA CGTGCCCCCC 300
TCTAAGTGCG CGCAGCCGGT CTTCCTGCTG CTGGTGATCA AGTCCTCCCC TAGCAACTAT 360
GTGCGCCGCG AGCTGCTGCG GCGCACGTGG GGCCGCGAGC GCAAGGTACG GGGTTTGCAG 420
CTGCGCCTCC TCTTCCTGGT GGGCACAGCC TCCAACCCGC ACGAGGCCCG CAAGGTCAAC 480
CGGCTGCTGG AGCTGGAGGC ACAGACTCAC GGAGACATCC TGCAGTGGGA CTTCCACGAC 540
TCCTTCTTCA ACCTCACGCT CAAGCAGGTC CTGTTCTTAC AGTGGCAGGA GACAAGGTGC 600
GCCAACGCCA GCTTCGTGCT CAACGGGGAT GATGACGTCT TTGCACACAC AGACAACATG 660
GTCTTCTACC TGCAGGACCA TGACCCTGGC CGCCACCTCT TCGTGGGGCA ACTGATCCAA 720
AACGTGGGCC CCATCCGGGC TTTTTGGAGC AAGTACTATG TGCCAGAGGT GGTGACTCAG 780
AATGAGCGGT ACCCACCCTA TTGTGGGGGT GGTGGCTTCT TGCTGTCCCG CTTCACGGCC 840
GCTGCCCTGC GCCGTGCTGC CCATGTCTTG GACATCTTCC CCATTGATGA TGTCTTCCTG 900
GGTATGTGTC TGGAGCTTGA GGGACTGAAG CCTGCCTCCC ACAGCGGCAT CCGCACGTCT 960
GGCGTGCGGG CTCCATCGCA ACACCTGTCC TCCTTTGACC CCTGCTTCTA CCGAGACCTG 1020
CTGCTGGTGC ACCGCTTCCT ACCTTATGAG ATGCTGCTCA TGTGGGATGC GCTGAACCAG 1080
CCCAACCTCA CCTGCGGCAA TCAGACACAG ATCTAC 1116

Sequence No.: 51
Sequence length: 986
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Fibrosarcoma
  Cell line: HT-1080
  Clone name: HP00442
Sequence characteristics
  Code representing characteristics: CDS
  Existence site: 82.. 699
  Characterization method: E
Sequence description

AGACTGCGGG ACGGACGGTG GACGCTGGGA CGCGTTTGTA GCTCCGGCCC CGCCGTTCCG 60
ACCCCCGCCG CCGTCGCCGC C ATG ACG GGG CTA GCA CTG CTC TAC TCC GGG 111
Met Thr Gly Leu Ala Leu Leu Tyr Ser Gly
1 5 10
GTC TTC GTG GCC TTC TGG GCC TGC GCG CTG GCC GTG GGA GTC TGC TAC 159
Val Phe Val Ala Phe Trp Ala Cys Ala Leu Ala Val Gly Val Cys Tyr
15 20 25
ACC ATT TTT GAT TTG GGC TTC CGC TTT GAT GTG GCA TGG TTC CTG ACG 207
Thr Ile Phe Asp Leu Gly Phe Arg Phe Asp Val Ala Trp Phe Leu Thr

```
                30                   35                   40
GAG ACT TCG CCC TTC ATG TGG TCC AAC CTG GGC ATT GGC CTA GCT ATC      255
Glu Thr Ser Pro Phe Met Trp Ser Asn Leu Gly Ile Gly Leu Ala Ile
            45                   50                   55
TCC CTG TCT GTG GTT GGG GCA GCC TGG GGC ATC TAT ATT ACC GGC TCC      303
Ser Leu Ser Val Val Gly Ala Ala Trp Gly Ile Tyr Ile Thr Gly Ser
        60                   65                   70
TCC ATC ATT GGT GGA GGA GTG AAG GCC CCC AGG ATC AAG ACC AAG AAC      351
Ser Ile Ile Gly Gly Gly Val Lys Ala Pro Arg Ile Lys Thr Lys Asn
    75                   80                   85                   90
CTG GTC AGC ATC ATC TTC TGT GAG GCT GTG GCC ATC TAC GGC ATC ATC      399
Leu Val Ser Ile Ile Phe Cys Glu Ala Val Ala Ile Tyr Gly Ile Ile
                    95                  100                  105
ATG GCA ATT GTC ATT AGC AAC ATG GCT GAG CCT TTC AGT GCC ACA GAC      447
Met Ala Ile Val Ile Ser Asn Met Ala Glu Pro Phe Ser Ala Thr Asp
                110                  115                  120
CCC AAG GCC ATC GGC CAT CGG AAC TAC CAT GCA GGC TAC TCC ATG TTT      495
Pro Lys Ala Ile Gly His Arg Asn Tyr His Ala Gly Tyr Ser Met Phe
            125                  130                  135
GGG GCT GGC CTC ACC GTA GGC CTG TCT AAC CTC TTC TGT GGA GTC TGC      543
Gly Ala Gly Leu Thr Val Gly Leu Ser Asn Leu Phe Cys Gly Val Cys
        140                  145                  150
GTG GGC ATC GTG GGC AGT GGG GCT GCC CTG GCC GAT GCT CAG AAC CCC      591
Val Gly Ile Val Gly Ser Gly Ala Ala Leu Ala Asp Ala Gln Asn Pro
155                  160                  165                  170
AGC CTC TTT GTA AAG ATT CTC ATC GTG GAG ATC TTT GGC AGC GCC ATT      639
Ser Leu Phe Val Lys Ile Leu Ile Val Glu Ile Phe Gly Ser Ala Ile
                175                  180                  185
GGC CTC TTT GGG GTC ATC GTC GCA ATT CTT CAG ACC TCC AGA GTG AAG      687
Gly Leu Phe Gly Val Ile Val Ala Ile Leu Gln Thr Ser Arg Val Lys
                190                  195                  200
ATG GGT GAC TAGATGATAT GTGTGGGTGG GGCCGTGCCT CACT                    730
Met Gly Asp
        205
TTTATTTATT GCTGGTTTTC CTGGGACAGC TGGAGCTGTG TCCCTTAGCC TTTCAGAGGC    790
TTGGTGTTCA GGGCCCTCCC TGCACTCCCC TCTTGCTGCG TGTTGATTTG GAGGCACTGC    850
AGTCCAGGCC GAGTCCTCAG TGCGGGGAGC AGGCTGCTGC TGCTGACTCT GTGCAGCTGC    910
GCACCTGTGT CCCCCACCTC CACCCTCAAC CCATCTTCCT AGTGTTTGTG AAATAAACTT    970
GGTATTTGTC TGGGTC                                                    986
```

Sequence No.: 52

Sequence length: 1824

Sequence type: Nucleic acid

Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Leukocyte
  Clone name: HP00804
Sequence characteristics
  Code representing characteristics: CDS
  Existence site: 133.. 1248
  Characterization method: E
Sequence description

```
GGCCCAGCTG AGCGGCCGCC GAGCGGGTGC GGGTGCGGGC GCATCGGCCA TCACCGCGCG    60
GCCGCGCAGC GGACACCGTG CGTACCGGCC TGCGGCGCCC GGCCACCGGG GCGGACCGCG   120
GAACCCGAGG CC ATG TCC CAT GAA AAG AGT TTT TTG GTG TCT GGG GAC AAC   171
              Met Ser His Glu Lys Ser Phe Leu Val Ser Gly Asp Asn
                1               5                  10
TAT CCT CCC CCC AAC CCT GGA TAT CCG GGG GGG CCC CAG CCA CCC ATG     219
Tyr Pro Pro Pro Asn Pro Gly Tyr Pro Gly Gly Pro Gln Pro Pro Met
    15                  20                  25
CCC CCC TAT GCT CAG CCT CCC TAC CCT GGG GCC CCT TAC CCA CAG CCC     267
Pro Pro Tyr Ala Gln Pro Pro Tyr Pro Gly Ala Pro Tyr Pro Gln Pro
30                  35                  40                  45
CCT TTC CAG CCC TCC CCC TAC GGT CAG CCA GGG TAC CCC CAT GGC CCC     315
Pro Phe Gln Pro Ser Pro Tyr Gly Gln Pro Gly Tyr Pro His Gly Pro
                50                  55                  60
AGC CCC TAC CCC CAA GGG GGC TAC CCA CAG GGT CCC TAC CCC CAA GGG     363
Ser Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Gly
            65                  70                  75
GGC TAC CCA CAG GGC CCC TAC CCA CAA GAG GGC TAC CCA CAG GGC CCC     411
Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Glu Gly Tyr Pro Gln Gly Pro
        80                  85                  90
TAC CCC CAA GGG GGC TAC CCC CAG GGG CCA TAT CCC CAG AGC CCC TTC     459
Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Ser Pro Phe
    95                  100                 105
CCC CCC AAC CCC TAT GGA CAG CCA CAG GTC TTC CCA GGA CAA GAC CCT     507
Pro Pro Asn Pro Tyr Gly Gln Pro Gln Val Phe Pro Gly Gln Asp Pro
110                 115                 120                 125
GAC TCA CCC CAG CAT GGA AAC TAC CAG GAG GAG GGT CCC CCA TCC TAC     555
Asp Ser Pro Gln His Gly Asn Tyr Gln Glu Glu Gly Pro Pro Ser Tyr
                130                 135                 140
TAT GAC AAC CAG GAC TTC CCT GCC ACC AAC TGG GAT GAC AAG AGC ATC     603
Tyr Asp Asn Gln Asp Phe Pro Ala Thr Asn Trp Asp Asp Lys Ser Ile
```

```
          145                 150                 155
CGA CAG GCC TTC ATC CGC AAG GTG TTC CTA GTG CTG ACC TTG CAG CTG      651
Arg Gln Ala Phe Ile Arg Lys Val Phe Leu Val Leu Thr Leu Gln Leu
        160                 165                 170
TCG GTG ACC CTG TCC ACG GTG TCT GTG TTC ACT TTT GTT GCG GAG GTG      699
Ser Val Thr Leu Ser Thr Val Ser Val Phe Thr Phe Val Ala Glu Val
    175                 180                 185
AAG GGC TTT GTC CGG GAG AAT GTC TGG ACC TAC TAT GTC TCC TAT GCT      747
Lys Gly Phe Val Arg Glu Asn Val Trp Thr Tyr Tyr Val Ser Tyr Ala
190                 195                 200                 205
GTC TTC TTC ATC TCT CTC ATC GTC CTC AGC TGT TGT GGG GAC TTC CGG      795
Val Phe Phe Ile Ser Leu Ile Val Leu Ser Cys Cys Gly Asp Phe Arg
                210                 215                 220
CGA AAG CAC CCC TGG AAC CTT GTT GCA CTG TCG GTC CTG ACC GCC AGC      843
Arg Lys His Pro Trp Asn Leu Val Ala Leu Ser Val Leu Thr Ala Ser
            225                 230                 235
CTG TCG TAC ATG GTG GGG ATG ATC GCC AGC TTC TAC AAC ACC GAG GCA      891
Leu Ser Tyr Met Val Gly Met Ile Ala Ser Phe Tyr Asn Thr Glu Ala
        240                 245                 250
GTC ATC ATG GCC GTG GGC ATC ACC ACA GCC GTC TGC TTC ACC GTC GTC      939
Val Ile Met Ala Val Gly Ile Thr Thr Ala Val Cys Phe Thr Val Val
    255                 260                 265
ATC TTC TCC ATG CAG ACC CGC TAC GAC TTC ACC TCA TGC ATG GGC GTG      987
Ile Phe Ser Met Gln Thr Arg Tyr Asp Phe Thr Ser Cys Met Gly Val
270                 275                 280                 285
CTC CTG GTG AGC ATG GTG GTG CTC TTC ATC TTC GCC ATT CTC TGC ATC     1035
Leu Leu Val Ser Met Val Val Leu Phe Ile Phe Ala Ile Leu Cys Ile
                290                 295                 300
TTC ATC CGG AAC CGC ATC CTG GAG ATC GTG TAC GCC TCA CTG GGC GCT     1083
Phe Ile Arg Asn Arg Ile Leu Glu Ile Val Tyr Ala Ser Leu Gly Ala
            305                 310                 315
CTG CTC TTC ACC TGC TTC CTC GCA GTG GAC ACC CAG CTG CTG CTG GGG     1131
Leu Leu Phe Thr Cys Phe Leu Ala Val Asp Thr Gln Leu Leu Leu Gly
        320                 325                 330
AAC AAG CAG CTG TCC CTG AGC CCA GAA GAG TAT GTG TTT GCT GCG CTG     1179
Asn Lys Gln Leu Ser Leu Ser Pro Glu Glu Tyr Val Phe Ala Ala Leu
    335                 340                 345
AAC CTG TAC ACA GAC ATC ATC AAC ATC TTC CTG TAC ATC CTC ACC ATC     1227
Asn Leu Tyr Thr Asp Ile Ile Asn Ile Phe Leu Tyr Ile Leu Thr Ile
350                 355                 360                 365
ATT GGC CGC GCC AAG GAG TAGCCGAGCT CCAGCTCGCT GTGCC                 1270
Ile Gly Arg Ala Lys Glu
                370
CGCTCAGGTG GCACGGCTGG CCTGGACCCT GCCCCTGGCA CGGCAGTGCC AGCTGTACTT   1330
```

CCCCTCTCTC TTGTCCCCAG GCACAGCCTA GGGAAAAGGA TGCCTCTCTC CAACCCTCCT 1390
GTATGTACAC TGCAGATACT TCCATTTGGA CCCGCTGTGG CCACAGCATG GCCCCTTTAG 1450
TCCTCCCGCC CCCGCCAAGG GGCACCAAGG CCACGTTTCC GTGCCACCTC CTGTCTACTC 1510
ATTGTTGCAT GAGCCCTGTC TGCCAGCCCA CCCCAGGGAC TGGGGGCAGC ACCAGGTCCC 1570
GGGGAGAGGG ATTGAGCCAA GAGGTGAGGG TGCACGTCTT CCCTCCTGTC CCAGCTCCCC 1630
AGCCTGGCGT AGAGCACCCC TCCCCTCCCC CCCACCCCCC TGGAGTGCTG CCCTCTGGGG 1690
ACATGCGGAG TGGGGGTCTT ATCCCTGTGC TGAGCCCTGA GGGCAGAGAG GATGGCATGT 1750
TTCAGGGGAG GGGGAAGCCT TCCTCTCAAT TTGTTGTCAG TGAAATTCCA ATAAATGGGA 1810
TTTGCTCTCT GCCT 1824

Sequence No.: 53
Sequence length: 1076
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Stomach cancer
  Clone name: HP01098
Sequence characteristics
  Code representing characteristics: CDS
  Existence site: 62.. 601
  Characterization method: E
Sequence description

AGTTCCGCCC GCTGGTCATC GCGCCCTTTC CCCTGCCGGT GTCCTGCTCG CCGTCCCCGC 60
C ATG CTG TCT CTA GAC TTT TTG GAC GAT GTG CGG CGG ATG AAC AAG CGG 109
Met Leu Ser Leu Asp Phe Leu Asp Asp Val Arg Arg Met Asn Lys Arg
1 5 10 15
CAG CTC TAT TAT CAA GTC CTA AAT TTT GGA ATG ATT GTC TCA TCG GCA 157
Gln Leu Tyr Tyr Gln Val Leu Asn Phe Gly Met Ile Val Ser Ser Ala
20 25 30
CTA ATG ATC TGG AAG GGG TTA ATG GTA ATA ACT GGA AGT GAA AGT CCG 205
Leu Met Ile Trp Lys Gly Leu Met Val Ile Thr Gly Ser Glu Ser Pro
35 40 45
ATT GTA GTG GTG CTC AGT GGC AGC ATG GAA CCT GCA TTT CAT AGA GGA 253
Ile Val Val Val Leu Ser Gly Ser Met Glu Pro Ala Phe His Arg Gly
50 55 60
GAT CTT CTC TTT CTA ACA AAT CGA GTT GAA GAT CCC ATA CGA GTG GGA 301
Asp Leu Leu Phe Leu Thr Asn Arg Val Glu Asp Pro Ile Arg Val Gly
65 70 75 80
GAA ATT GTT GTT TTT AGG ATA GAA GGA AGA GAG ATT CCT ATA GTT CAC 349

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Glu Ile Val Val Phe Arg Ile Glu Gly Arg Glu Ile Pro Ile Val His
                 85                  90                  95
CGA GTC TTG AAG ATT CAT GAA AAG CAA AAT GGG CAT ATC AAG TTT TTG      397
Arg Val Leu Lys Ile His Glu Lys Gln Asn Gly His Ile Lys Phe Leu
            100                 105                 110
ACC AAA GGA GAT AAT AAT GCG GTT GAT GAC CGA GGC CTC TAT AAA CAA      445
Thr Lys Gly Asp Asn Asn Ala Val Asp Asp Arg Gly Leu Tyr Lys Gln
        115                 120                 125
GGA CAA CAT TGG CTA GAG AAA AAA GAT GTT GTG GGG AGA GCC AGG GGA      493
Gly Gln His Trp Leu Glu Lys Lys Asp Val Val Gly Arg Ala Arg Gly
    130                 135                 140
TTT GTT CCT TAT ATT GGA ATT GTG ACG ATC CTC ATG AAT GAC TAT CCT      541
Phe Val Pro Tyr Ile Gly Ile Val Thr Ile Leu Met Asn Asp Tyr Pro
145                 150                 155                 160
AAA TTT AAG TAT GCA GTT CTC TTT TTG CTG GGT TTA TTC GTG CTG GTT      589
Lys Phe Lys Tyr Ala Val Leu Phe Leu Leu Gly Leu Phe Val Leu Val
                165                 170                 175
CAT CGT GAG TA AGAAGCC TGCCTTGCTG TTCCTGGGAA GAT                     630
His Arg Glu

GCCATAGTTT TCGTTACTGG ATGTTTGGAG TAGATACTGG TCTGTGATTG GTGGAATGGA    690
GAACACACGT GTTGGTGCTT CTGGGTAGCA CTGGTTTGCA TTAGTTTATG TTTCCATGCC    750
AGAGTTTGTG TGGGCGGGCG CATGTGCACC ACAGAGTGCA CTCGAGGGGA CTTTCAGTCA    810
CAGGATTTCA TAATTGTCAT TGTCACACTT TCAAATTTTT GTACATCAGT GAATTTTTTT    870
ATATTAAAAG GTTGAGCCAA AGCCCCCAGT GTTTGTATTT TGAAGCCAAG CTTCACTTCT    930
AAAGTGCCTA CAGAGACTTG TAAATGAAAA TGCAGCTCTG CACGAGTTTG AAACCGTCAT    990
ACCTCCTTCT ATTAGGAATG GCATATACTG AGGTGGTCGT AAGTCTTAAC TTCTAAAATT   1050
TTAAATAAAA GACTTTGCAC ATTGAG                                         1076
```

Sequence No.: 54

Sequence length: 1591

Sequence type: Nucleic acid

Strandedness: Double

Topology: Linear

Sequence kind: cDNA to mRNA

Original source:

  Organism species: *Homo sapiens*

  Cell kind: Liver

  Clone name: HP01148

Sequence characteristics

  Code representing characteristics: CDS

  Existence site: 102.. 1145

  Characterization method: E

Sequence description

```
GTCCCTCCTC TTAACATACT TGCAGCTAAA ACTAAATATT GCTGCTTGGG GACCTCCTTC    60
TAGCCTTAAA TTTCAGCTCA TCACCTTCAC CTGCCTTGGT C ATG GCT CTG CTA TTC   116
                                              Met Ala Leu Leu Phe
                                                1               5
TCC TTG ATC CTT GCC ATT TGC ACC AGA CCT GGA TTC CTA GCG TCT CCA     164
Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly Phe Leu Ala Ser Pro
                 10                  15                  20
TCT GGA GTG CGG CTG GTG GGG GGC CTC CAC CGC TGT GAA GGG CGG GTG     212
Ser Gly Val Arg Leu Val Gly Gly Leu His Arg Cys Glu Gly Arg Val
             25                  30                  35
GAG GTG GAA CAG AAA GGC CAG TGG GGC ACC GTG TGT GAT GAC GGC TGG     260
Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val Cys Asp Asp Gly Trp
         40                  45                  50
GAC ATT AAG GAC GTG GCT GTG TTG TGC CGG GAG CTG GGC TGT GGA GCT     308
Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu Leu Gly Cys Gly Ala
     55                  60                  65
GCC AGC GGA ACC CCT AGT GGT ATT TTG TAT GAG CCA CCA GCA GAA AAA     356
Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu Pro Pro Ala Glu Lys
 70                  75                  80                  85
GAG CAA AAG GTC CTC ATC CAA TCA GTC AGT TGC ACA GGA ACA GAA GAT     404
Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys Thr Gly Thr Glu Asp
                 90                  95                 100
ACA TTG GCT CAG TGT GAG CAA GAA GAA GTT TAT GAT TGT TCA CAT GAA     452
Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr Asp Cys Ser His Glu
            105                 110                 115
GAA GAT GCT GGG GCA TCG TGT GAG AAC CCA GAG AGC TCT TTC TCC CCA     500
Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu Ser Ser Phe Ser Pro
        120                 125                 130
GTC CCA GAG GGT GTC AGG CTG GCT GAC GGC CCT GGG CAT TGC AAG GGA     548
Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro Gly His Cys Lys Gly
    135                 140                 145
CGC GTG GAA GTG AAG CAC CAG AAC CAG TGG TAT ACC GTG TGC CAG ACA     596
Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr Thr Val Cys Gln Thr
150                 155                 160                 165
GGC TGG AGC CTC CGG GCC GCA AAG GTG GTG TGC CGG CAG CTG GGA TGT     644
Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys Arg Gln Leu Gly Cys
                170                 175                 180
GGG AGG GCT GTA CTG ACT CAA AAA CGC TGC AAC AAG CAT GCC TAT GGC     692
Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn Lys His Ala Tyr Gly
            185                 190                 195
CGA AAA CCC ATC TGG CTG AGC CAG ATG TCA TGC TCA GGA CGA GAA GCA     740
Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys Ser Gly Arg Glu Ala
```

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        200                 205                 210
ACC CTT CAG GAT TGC CCT TCT GGG CCT TGG GGG AAG AAC ACC TGC AAC      788
Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly Lys Asn Thr Cys Asn
    215                 220                 225
CAT GAT GAA GAC ACG TGG GTC GAA TGT GAA GAT CCC TTT GAC TTG AGA      836
His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp Pro Phe Asp Leu Arg
230                 235                 240                 245
CTA GTA GGA GGA GAC AAC CTC TGC TCT GGG CGA CTG GAG GTG CTG CAC      884
Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg Leu Glu Val Leu His
                250                 255                 260
AAG GGC GTA TGG GGC TCT GTC TGT GAT GAC AAC TGG GGA GAA AAG GAG      932
Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn Trp Gly Glu Lys Glu
            265                 270                 275
GAC CAG GTG GTA TGC AAG CAA CTG GGC TGT GGG AAG TCC CTC TCT CCC      980
Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly Lys Ser Leu Ser Pro
        280                 285                 290
TCC TTC AGA GAC CGG AAA TGC TAT GGC CCT GGG GTT GGC CGC ATC TGG     1028
Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly Val Gly Arg Ile Trp
    295                 300                 305
CTG GAT AAT GTT CGT TGC TCA GGG GAG GAG CAG TCC CTG GAG CAG TGC     1076
Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln Ser Leu Glu Gln Cys
310                 315                 320                 325
CAG CAC AGA TTT TGG GGG TTT CAC GAC TGC ACC CAC CAG GAA GAT GTG     1124
Gln His Arg Phe Trp Gly Phe His Asp Cys Thr His Gln Glu Asp Val
                330                 335                 340
GCT GTC ATC TGC TCA GGA TAGTATCCTG GTGTTGCTTG ACCTGGCC              1170
Ala Val Ile Cys Ser Gly
            345
CCCCTGGCCC CGCCTGCCCT CTGCTTGTTC TCCTGAGCCC TGATTATCCT CATACTCATT   1230
CTGGGGCTCA GGCTTGAGCC ACTACTCCCT CATCCCCTCA GGAGTCTGAA CACTGGGCTT   1290
ATGCCTTACT CTCAGGGACA AGCAGCCCCC ATTGCTGCCT GTAGATGTGA GCTGTTGAGT   1350
TCCCTCTTGC TGGGGAAGAT GAGCTTCCAT GTATCCTGTG CTCAACCCTG ACCCTTTGAC   1410
ACTGGTTCTG GCCTTTCCTG CCTTTTCTCA AGCTGCCTGG AATCCTCAAA CCTGTCACTT   1470
TGGTCAGATG TGCAGACCAT TACTAAGGTC TATGTCTGCA AACATTACTA ATCTAGGTCC   1530
TATTACTAAT CTATGTCTGC AAACATTAAA GGAATGAAAC AATGAAAGGA ACATTTGAAA   1590
G                                                                   1591
```

Sequence No.: 55
Sequence length: 1888
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA

Original source:
Organism species: *Homo sapiens*
Cell kind: Liver
Clone name: HP01293
Sequence characteristics
Code representing characteristics: CDS
Existence site: 90.. 1754
Characterization method: E
Sequence description

```
CCTTTTCAAA GATCTCTGAG GGAGACATTG CACCTGGCCA CTGCAGCCCA GAGCAGGTCT      60
GGCCACGGCC ATGAGCATGC TGAGCCATC ATG CCC ACC GTG GAT GAC ATT CTG      113
                                Met Pro Thr Val Asp Asp Ile Leu
                                  1               5
GAG CAG GTT GGG GAG TCT GGC TGG TTC CAG AAG CAA GCC TTC CTC ATC      161
Glu Gln Val Gly Glu Ser Gly Trp Phe Gln Lys Gln Ala Phe Leu Ile
     10                  15                  20
TTA TGC CTG CTG TCG GCT GCC TTT GCG CCC ATC TGT GTG GGC ATC GTC      209
Leu Cys Leu Leu Ser Ala Ala Phe Ala Pro Ile Cys Val Gly Ile Val
 25                  30                  35                  40
TTC CTG GGT TTC ACA CCT GAC CAC CAC TGC CAG AGT CCT GGG GTG GCT      257
Phe Leu Gly Phe Thr Pro Asp His His Cys Gln Ser Pro Gly Val Ala
                 45                  50                  55
GAG CTG AGC CAG CGC TGT GGC TGG AGC CCT GCG GAG GAG CTG AAC TAT      305
Glu Leu Ser Gln Arg Cys Gly Trp Ser Pro Ala Glu Glu Leu Asn Tyr
             60                  65                  70
ACA GTG CCA GGC CTG GGG CCC GCG GGC GAG GCC TTC CTT GGC CAG TGC      353
Thr Val Pro Gly Leu Gly Pro Ala Gly Glu Ala Phe Leu Gly Gln Cys
         75                  80                  85
AGG CGC TAT GAA GTG GAC TGG AAC CAG AGC GCC CTC AGC TGT GTA GAC      401
Arg Arg Tyr Glu Val Asp Trp Asn Gln Ser Ala Leu Ser Cys Val Asp
     90                  95                 100
CCC CTG GCT AGC CTG GCC ACC AAC AGG AGC CAC CTG CCG CTG GGT CCC      449
Pro Leu Ala Ser Leu Ala Thr Asn Arg Ser His Leu Pro Leu Gly Pro
105                 110                 115                 120
TGC CAG GAT GGC TGG GTG TAT GAC ACG CCC GGC TCT TCC ATC GTC ACT      497
Cys Gln Asp Gly Trp Val Tyr Asp Thr Pro Gly Ser Ser Ile Val Thr
                125                 130                 135
GAG TTC AAC CTG GTG TGT GCT GAC TCC TGG AAG CTG GAC CTC TTT CAG      545
Glu Phe Asn Leu Val Cys Ala Asp Ser Trp Lys Leu Asp Leu Phe Gln
            140                 145                 150
TCC TGT TTG AAT GCG GGC TTC TTC TTT GGC TCT CTC GGT GTT GGC TAC      593
Ser Cys Leu Asn Ala Gly Phe Phe Phe Gly Ser Leu Gly Val Gly Tyr
        155                 160                 165
```

TTT GCA GAC AGG TTT GGC CGT AAG CTG TGT CTC CTG GGA ACT GTG CTG 641
Phe Ala Asp Arg Phe Gly Arg Lys Leu Cys Leu Leu Gly Thr Val Leu
170 175 180

GTC AAC GCG GTG TCG GGC GTG CTC ATG GCC TTC TCG CCC AAC TAC ATG 689
Val Asn Ala Val Ser Gly Val Leu Met Ala Phe Ser Pro Asn Tyr Met
185 190 195 200

TCC ATG CTG CTC TTC CGC CTG CTG CAG GGC CTG GTC AGC AAG GGC AAC 737
Ser Met Leu Leu Phe Arg Leu Leu Gln Gly Leu Val Ser Lys Gly Asn
205 210 215

TGG ATG GCT GGC TAC ACC CTA ATC ACA GAA TTT GTT GGC TCG GGC TCC 785
Trp Met Ala Gly Tyr Thr Leu Ile Thr Glu Phe Val Gly Ser Gly Ser
220 225 230

AGA AGA ACG GTG GCG ATC ATG TAC CAG ATG GCC TTC ACG GTG GGG CTG 833
Arg Arg Thr Val Ala Ile Met Tyr Gln Met Ala Phe Thr Val Gly Leu
235 240 245

GTG GCG CTT ACC GGG CTG GCC TAC GCC CTG CCT CAC TGG CGC TGG CTG 881
Val Ala Leu Thr Gly Leu Ala Tyr Ala Leu Pro His Trp Arg Trp Leu
250 255 260

CAG CTG GCA GTC TCC CTG CCC ACC TTC CTC TTC CTG CTC TAC TAC TGG 929
Gln Leu Ala Val Ser Leu Pro Thr Phe Leu Phe Leu Leu Tyr Tyr Trp
265 270 275 280

TGT GTG CCG GAG TCC CCT CGG TGG CTG TTA TCA CAA AAA AGA AAC ACT 977
Cys Val Pro Glu Ser Pro Arg Trp Leu Leu Ser Gln Lys Arg Asn Thr
285 290 295

GAA GCA ATA AAG ATA ATG GAC CAC ATC GCT CAA AAG AAT GGG AAG TTG 1025
Glu Ala Ile Lys Ile Met Asp His Ile Ala Gln Lys Asn Gly Lys Leu
300 305 310

CCT CCT GCT GAT TTA AAG ATG CTT TCC CTC GAA GAG GAT GTC ACC GAA 1073
Pro Pro Ala Asp Leu Lys Met Leu Ser Leu Glu Glu Asp Val Thr Glu
315 320 325

AAG CTG AGC CCT TCA TTT GCA GAC CTG TTC CGC ACG CCG CGC CTG AGG 1121
Lys Leu Ser Pro Ser Phe Ala Asp Leu Phe Arg Thr Pro Arg Leu Arg
330 335 340

AAG CGC ACC TTC ATC CTG ATG TAC CTG TGG TTC ACG GAC TCT GTG CTC 1169
Lys Arg Thr Phe Ile Leu Met Tyr Leu Trp Phe Thr Asp Ser Val Leu
345 350 355 360

TAT CAG GGG CTC ATC CTG CAC ATG GGC GCC ACC AGC GGG AAC CTC TAC 1217
Tyr Gln Gly Leu Ile Leu His Met Gly Ala Thr Ser Gly Asn Leu Tyr
365 370 375

CTG GAT TTC CTT TAC TCC GCT CTG GTC GAA ATC CCG GGG GCC TTC ATA 1265
Leu Asp Phe Leu Tyr Ser Ala Leu Val Glu Ile Pro Gly Ala Phe Ile
380 385 390

GCC CTC ATC ACC ATT GAC CGC GTG GGC CGC ATC TAC CCC ATG GCC GTG 1313
Ala Leu Ile Thr Ile Asp Arg Val Gly Arg Ile Tyr Pro Met Ala Val

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        395                 400                 405
TCA AAT TTG TTG GCG GGG GCA GCC TGC CTC GTC ATG ATT TTT ATC TCA      1361
Ser Asn Leu Leu Ala Gly Ala Ala Cys Leu Val Met Ile Phe Ile Ser
    410                 415                 420
CCT GAC CTG CAC TGG TTA AAC ATC ATA ATC ATG TGT GTT GGC CGA ATG      1409
Pro Asp Leu His Trp Leu Asn Ile Ile Ile Met Cys Val Gly Arg Met
425                 430                 435                 440
GGA ATC ACC ATT GCA ATA CAA ATG ATC TGC CTG GTG AAT GCT GAG CTG      1457
Gly Ile Thr Ile Ala Ile Gln Met Ile Cys Leu Val Asn Ala Glu Leu
                445                 450                 455
TAC CCC ACA TTC GTC AGG AAC CTC GGA GTG ATG GTG TGT TCC TCC CTG      1505
Tyr Pro Thr Phe Val Arg Asn Leu Gly Val Met Val Cys Ser Ser Leu
            460                 465                 470
TGT GAC ATA GGT GGG ATA ATC ACC CCC TTC ATA GTC TTC AGG CTG AGG      1553
Cys Asp Ile Gly Gly Ile Ile Thr Pro Phe Ile Val Phe Arg Leu Arg
        475                 480                 485
GAG GTC TGG CAA GCC TTG CCC CTC ATT TTG TTT GCG GTG TTG GGC CTG      1601
Glu Val Trp Gln Ala Leu Pro Leu Ile Leu Phe Ala Val Leu Gly Leu
    490                 495                 500
CTT GCC GCG GGA GTG ACG CTA CTT CTT CCA GAG ACC AAG GGG GTC GCT      1649
Leu Ala Ala Gly Val Thr Leu Leu Leu Pro Glu Thr Lys Gly Val Ala
505                 510                 515                 520
TTG CCA GAG ACC ATG AAG GAC GCC GAG AAC CTT GGG AGA AAA GCA AAG      1697
Leu Pro Glu Thr Met Lys Asp Ala Glu Asn Leu Gly Arg Lys Ala Lys
                525                 530                 535
CCC AAA GAA AAC ACG ATT TAC CTT AAG GTC CAA ACC TCA GAA CCC TCG      1745
Pro Lys Glu Asn Thr Ile Tyr Leu Lys Val Gln Thr Ser Glu Pro Ser
            540                 545                 550
GGC ACC TGAGAGAGAT GTTTTGCGGC GATGTCGTGT TGGAGGGATG AAGATGGAG        1800
Gly Thr

TTATCCTCTG CAGAAATTCC TAGACGCCTT CACTTCTCTG TATTCTTCCT CATACTTGCC    1860
TACCCCCAAA TTAATATCAG TCCTAAAG                                       1888
```

Sequence No.: 56
Sequence length: 2033
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Epidermoid carcinoma

Cell line: KB
Clone name: HP10013
Sequence characteristics
Code representing characteristics: CDS
Existence site: 97.. 1149
Characterization method: E
Sequence description

```
GAGTCCGAGC GCGTCACCTC CTCACGCTGC GGCTGTCGCC CGTGTCCCGC CGGCCCGTTC      60
CGTGTCGCCC CGCAGTGCTG CGGCCGCCGC GGCACC ATG GCT GTG TTT GTC GTG      114
                                        Met Ala Val Phe Val Val
                                          1               5
CTC CTG GCG TTG GTG GCG GGT GTT TTG GGG AAC GAG TTT AGT ATA TTA      162
Leu Leu Ala Leu Val Ala Gly Val Leu Gly Asn Glu Phe Ser Ile Leu
            10                  15                  20
AAA TCA CCA GGG TCT GTT GTT TTC CGA AAT GGA AAT TGG CCT ATA CCA      210
Lys Ser Pro Gly Ser Val Val Phe Arg Asn Gly Asn Trp Pro Ile Pro
        25                  30                  35
GGA GAG CGG ATC CCA GAC GTG GCT GCA TTG TCC ATG GGC TTC TCT GTG      258
Gly Glu Arg Ile Pro Asp Val Ala Ala Leu Ser Met Gly Phe Ser Val
    40                  45                  50
AAA GAA GAC CTT TCT TGG CCA GGA CTC GCA GTG GGT AAC CTG TTT CAT      306
Lys Glu Asp Leu Ser Trp Pro Gly Leu Ala Val Gly Asn Leu Phe His
 55                  60                  65                  70
CGT CCT CGG GCT ACC GTC ATG GTG ATG GTG AAG GGA GTG AAC AAA CTG      354
Arg Pro Arg Ala Thr Val Met Val Met Val Lys Gly Val Asn Lys Leu
                 75                  80                  85
GCT CTA CCC CCA GGC AGT GTC ATT TCG TAC CCT TTG GAG AAT GCA GTT      402
Ala Leu Pro Pro Gly Ser Val Ile Ser Tyr Pro Leu Glu Asn Ala Val
            90                  95                 100
CCT TTT AGT CTT GAC AGT GTT GCA AAT TCC ATT CAC TCC TTA TTT TCT      450
Pro Phe Ser Leu Asp Ser Val Ala Asn Ser Ile His Ser Leu Phe Ser
        105                 110                 115
GAG GAA ACT CCT GTT GTT TTG CAG TTG GCT CCC AGT GAG GAA AGA GTG      498
Glu Glu Thr Pro Val Val Leu Gln Leu Ala Pro Ser Glu Glu Arg Val
    120                 125                 130
TAT ATG GTA GGG AAG GCA AAC TCA GTG TTT GAA GAC CTT TCA GTC ACC      546
Tyr Met Val Gly Lys Ala Asn Ser Val Phe Glu Asp Leu Ser Val Thr
135                 140                 145                 150
TTG CGC CAG CTC CGT AAT CGC CTG TTT CAA GAA AAC TCT GTT CTC AGT      594
Leu Arg Gln Leu Arg Asn Arg Leu Phe Gln Glu Asn Ser Val Leu Ser
                155                 160                 165
TCA CTC CCC CTC AAT TCT CTG AGT AGG AAC AAT GAA GTT GAC CTG CTC      642
Ser Leu Pro Leu Asn Ser Leu Ser Arg Asn Asn Glu Val Asp Leu Leu
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170 175 180
TTT CTT TCT GAA CTG CAA GTG CTA CAT GAT ATT TCA AGC TTG CTG TCT 690
Phe Leu Ser Glu Leu Gln Val Leu His Asp Ile Ser Ser Leu Leu Ser
185 190 195
CGT CAT AAG CAT CTA GCC AAG GAT CAT TCT CCT GAT TTA TAT TCA CTG 738
Arg His Lys His Leu Ala Lys Asp His Ser Pro Asp Leu Tyr Ser Leu
200 205 210
GAG CTG GCA GGT TTG GAT GAA ATT GGG AAG CGT TAT GGG GAA GAC TCT 786
Glu Leu Ala Gly Leu Asp Glu Ile Gly Lys Arg Tyr Gly Glu Asp Ser
215 220 225 230
GAA CAA TTC AGA GAT GCT TCT AAG ATC CTT GTT GAC GCT CTG CAA AAG 834
Glu Gln Phe Arg Asp Ala Ser Lys Ile Leu Val Asp Ala Leu Gln Lys
235 240 245
TTT GCA GAT GAC ATG TAC AGT CTT TAT GGT GGG AAT GCA GTG GTA GAG 882
Phe Ala Asp Asp Met Tyr Ser Leu Tyr Gly Gly Asn Ala Val Val Glu
250 255 260
TTA GTC ACT GTC AAG TCA TTT GAC ACC TCC CTC ATT AGG AAG ACA AGG 930
Leu Val Thr Val Lys Ser Phe Asp Thr Ser Leu Ile Arg Lys Thr Arg
265 270 275
ACT ATC CTT GAG GCA AAA CAA GCG AAG AAC CCA GCA AGT CCC TAT AAC 978
Thr Ile Leu Glu Ala Lys Gln Ala Lys Asn Pro Ala Ser Pro Tyr Asn
280 285 290
CTT GCA TAT AAG TAT AAT TTT GAA TAT TCC GTG GTT TTC AAC ATG GTA 1026
Leu Ala Tyr Lys Tyr Asn Phe Glu Tyr Ser Val Val Phe Asn Met Val
295 300 305 310
CTT TGG ATA ATG ATC GCC TTG GCC TTG GCT GTG ATT ATC ACC TCT TAC 1074
Leu Trp Ile Met Ile Ala Leu Ala Leu Ala Val Ile Ile Thr Ser Tyr
315 320 325
AAT ATT TGG AAC ATG GAT CCT GGA TAT GAT AGC ATC ATT TAT AGG ATG 1122
Asn Ile Trp Asn Met Asp Pro Gly Tyr Asp Ser Ile Ile Tyr Arg Met
330 335 340
ACA AAC CAG AAG ATT CGA ATG GAT TGAATGTTAC CTGTGCCAGA ATTA 1170
Thr Asn Gln Lys Ile Arg Met Asp
345 350
GAAAAGGGGG TTGGAAATTG GCTGTTTTGT TAAAATATAT CTTTTAGTGT GCTTTAAAGT 1230
AGATAGTATA CTTTACATTT ATAAAAAAAA ATCAAATTTT GTTCTTTATT TTGTGTGTGC 1290
CTGTGATGTT TTTCTAGAGT GAATTATAGT ATTGACGTGA ATCCCACTGT GGTATAGATT 1350
CCATAATATG CTTGAATATT ATGATATAGC CATTTAATAA CATTGATTTC ATTCTGTTTA 1410
ATGAATTTGG AAATATGCAC TGAAAGAAAT GTAAAACATT TAGAATAGCT CGTGTTATGG 1470
AAAAAAGTGC ACTGAATTTA TTAGACAAAC TTACGAATGC TTAACTTCTT TACACAGCAT 1530
AGGTGAAAAT CATATTTGGG CTATTGTATA CTATGAACAA TTTGTAAATG TCTTAATTTG 1590
ATGTAAATAA CTCTGAAACA AGAGAAAAGG TTTTTAACTT AGAGTAGCCC TAAAATATGG 1650
ATGTGCTTAT ATAATCGCTT AGTTTTGGAA CTGTATCTGA GTAACAGAGG ACAGCTGTTT 1710
TTTAACCCTC TTCTGCAAGT TTGTTGACCT ACATGGGCTA ATATGGATAC TAAAAATACT 1770

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ACATTGATCT AAGAAGAAAC TAGCCTTGTG GAGTATATAG ATGCTTTTCA TTATACACAC   1830
AAAAATCCCT GAGGGACATT TTGAGGCATG AATATAAAAC ATTTTTATTT CAGTAACTTT   1890
TCCCCCTGTG TAAGTTACTA TGGTTTGTGG TACAACTTCA TTCTATAGAA TATTAAGTGG   1950
AAGTGGGTGA ATTCTACTTT TTATGTTGGA GTGGACCAAT GTCTATCAAG AGTGACAAAT   2010
AAAGTTAATG ATGATTCCAA AAC                                           2033
```

Sequence No.: 57
Sequence length: 911
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Fibrosarcoma
  Cell line: HT-1080
  Clone name: HP10034
Sequence characteristics
  Code representing characteristics: CDS
  Existence site: 176.. 805
  Characterization method: E
Sequence description

```
ACGCCTGGGT GACCTCTACG TATATACAGA GCCTCCCTGG CCCTCCTGGA AAGAGTCCTG     60
GAAAGACAAC CTTCAGGTCC AGCCCTGGAG CTGGAGGAGT GGAGCCCCAC TCTGAAGACG    120
CAGCCTTTCT CCAGGTTCTG TCTCTCCCAT TCTGATTCTT GACACCAGAT GCAGG ATG     178
                                                             Met
                                                               1
GTG TCC TCT CCC TGC ACG CAG GCA AGC TCA CGG ACT TGC TCC CGT ATC      226
Val Ser Ser Pro Cys Thr Gln Ala Ser Ser Arg Thr Cys Ser Arg Ile
              5                  10                  15
CTG GGA CTG AGC CTT GGG ACT GCA GCC CTG TTT GCT GCT GGG GCC AAC      274
Leu Gly Leu Ser Leu Gly Thr Ala Ala Leu Phe Ala Ala Gly Ala Asn
         20                  25                  30
GTG GCA CTC CTC CTT CCT AAC TGG GAT GTC ACC TAC CTG TTG AGG GGC      322
Val Ala Leu Leu Leu Pro Asn Trp Asp Val Thr Tyr Leu Leu Arg Gly
     35                  40                  45
CTC CTT GGC AGG CAT GCC ATG CTG GGA ACT GGG CTC TGG GGA GGA GGC      370
Leu Leu Gly Arg His Ala Met Leu Gly Thr Gly Leu Trp Gly Gly Gly
 50                  55                  60                  65
CTC ATG GTA CTC ACT GCA GCT ATC CTC ATC TCC TTG ATG GGC TGG AGA      418
Leu Met Val Leu Thr Ala Ala Ile Leu Ile Ser Leu Met Gly Trp Arg
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                70                  75                  80
TAC GGC TGC TTC AGT AAG AGT GGG CTC TGT CGA AGC GTG CTT ACT GCT      466
Tyr Gly Cys Phe Ser Lys Ser Gly Leu Cys Arg Ser Val Leu Thr Ala
            85                  90                  95
CTG TTG TCA GGT GGC CTG GCT TTA CTT GGA GCC CTG ATT TGC TTT GTC      514
Leu Leu Ser Gly Gly Leu Ala Leu Leu Gly Ala Leu Ile Cys Phe Val
        100                 105                 110
ACT TCT GGA GTT GCT CTG AAA GAT GGT CCT TTT TGC ATG TTT GAT GTT      562
Thr Ser Gly Val Ala Leu Lys Asp Gly Pro Phe Cys Met Phe Asp Val
    115                 120                 125
TCA TCC TTC AAT CAG ACA CAA GCT TGG AAA TAT GGT TAC CCA TTC AAA      610
Ser Ser Phe Asn Gln Thr Gln Ala Trp Lys Tyr Gly Tyr Pro Phe Lys
130                 135                 140                 145
GAC CTG CAT AGT AGG AAT TAT CTG TAT GAC CGT TCG CTC TGG AAC TCC      658
Asp Leu His Ser Arg Asn Tyr Leu Tyr Asp Arg Ser Leu Trp Asn Ser
                150                 155                 160
GTC TGC CTG GAG CCC TCT GCA GCT GTT GTC TGG CAC GTG TCC CTC TTC      706
Val Cys Leu Glu Pro Ser Ala Ala Val Val Trp His Val Ser Leu Phe
            165                 170                 175
TCC GCC CTT CTG TGC ATC AGC CTG CTC CAG CTT CTC CTG GTG GTC GTT      754
Ser Ala Leu Leu Cys Ile Ser Leu Leu Gln Leu Leu Leu Val Val Val
        180                 185                 190
CAT GTC ATC AAC AGC CTC CTG GGC CTT TTC TGC AGC CTC TGC GAG AAG      802
His Val Ile Asn Ser Leu Leu Gly Leu Phe Cys Ser Leu Cys Glu Lys
    195                 200                 205
TGACAGGC AGAACCTTCA CTTGCAAGCA TGGGTGTTTA TCATCATCGG CTGTCTTGAA      860
TCCTTTCTAC AAGGAGTGGG TACGAATTAT AAACAAACTT CCCCTTTAGG T             911
```

Sequence No.: 58
Sequence length: 601
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Fibrosarcoma
  Cell line: HT-1080
  Clone name: HP10050
Sequence characteristics
  Code representing characteristics: CDS
  Existence site: 10.. 501
  Characterization method: E

Sequence description

CCATCTGTC ATG GCG GCT GGG CTG TTT GGT TTG AGC GCT CGC CGT CTT TTG 51
Met Ala Ala Gly Leu Phe Gly Leu Ser Ala Arg Arg Leu Leu
1 5 10
GCG GCA GCG GCG ACG CGA GGG CTC CCG GCC GCC CGC GTC CGC TGG GAA 99
Ala Ala Ala Ala Thr Arg Gly Leu Pro Ala Ala Arg Val Arg Trp Glu
15 20 25 30
TCT AGC TTC TCC AGG ACT GTG GTC GCC CCG TCC GCT GTG GCG GGA AAG 147
Ser Ser Phe Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala Gly Lys
35 40 45
CGG CCC CCA GAA CCG ACC ACA CCG TGG CAA GAG GAC CCA GAA CCC GAG 195
Arg Pro Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu Pro Glu
50 55 60
GAC GAA AAC TTG TAT GAG AAG AAC CCA GAC TCC CAT GGT TAT GAC AAG 243
Asp Glu Asn Leu Tyr Glu Lys Asn Pro Asp Ser His Gly Tyr Asp Lys
65 70 75
GAC CCC GTT TTG GAC GTC TGG AAC ATG CGA CTT GTC TTC TTC TTT GGC 291
Asp Pro Val Leu Asp Val Trp Asn Met Arg Leu Val Phe Phe Phe Gly
80 85 90
GTC TCC ATC ATC CTG GTC CTT GGC AGC ACC TTT GTG GCC TAT CTG CCT 339
Val Ser Ile Ile Leu Val Leu Gly Ser Thr Phe Val Ala Tyr Leu Pro
95 100 105 110
GAC TAC AGG TGC ACA GGG TGT CCA AGA GCG TGG GAT GGG ATG AAA GAG 387
Asp Tyr Arg Cys Thr Gly Cys Pro Arg Ala Trp Asp Gly Met Lys Glu
115 120 125
TGG TCC CGC CGC GAA GCT GAG AGG CTT GTG AAA TAC CGA GAG GCC AAT 435
Trp Ser Arg Arg Glu Ala Glu Arg Leu Val Lys Tyr Arg Glu Ala Asn
130 135 140
GGC CTT CCC ATC ATG GAA TCC AAC TGC TTC GAC CCC AGC AAG ATC CAG 483
Gly Leu Pro Ile Met Glu Ser Asn Cys Phe Asp Pro Ser Lys Ile Gln
145 150 155
CTG CCA GAG GAT GAG TGACCAGTTG CTAAGTGGGG CTCAAGAAGC AC 530
Leu Pro Glu Asp Glu
160
CGCCTTCCCC ACCCCCTGCC TGCCATTCTG ACCTCTTCTC AGAGCACCTA ATTAAAGGGG 590
CTGAAAGTCT G 601

Sequence No.: 59
Sequence length: 394
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear

Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Stomach cancer
  Clone name: HP10071
Sequence characteristics
  Code representing characteristics: CDS
  Existence site: 47.. 325
  Characterization method: E
Sequence description

```
AACATCCGGG CCGCGCGGGG AAGGGGAGAC GTGGGGTAGA GTGACC ATG ACG AAA          55
                                                   Met Thr Lys
                                                    1
TTA GCG CAG TGG CTT TGG GGA CTA GCG ATC CTG GGC TCC ACC TGG GTG        103
Leu Ala Gln Trp Leu Trp Gly Leu Ala Ile Leu Gly Ser Thr Trp Val
     5                  10                  15
GCC CTG ACC ACG GGA GCC TTG GGC CTG GAG CTG CCC TTG TCC TGC CAG        151
Ala Leu Thr Thr Gly Ala Leu Gly Leu Glu Leu Pro Leu Ser Cys Gln
 20                  25                  30                  35
GAA GTC CTG TGG CCA CTG CCC GCC TAC TTG CTG GTG TCC GCC GGC TGC        199
Glu Val Leu Trp Pro Leu Pro Ala Tyr Leu Leu Val Ser Ala Gly Cys
                 40                  45                  50
TAT GCC CTG GGC ACT GTG GGC TAT CGT GTG GCC ACT TTT CAT GAC TGC        247
Tyr Ala Leu Gly Thr Val Gly Tyr Arg Val Ala Thr Phe His Asp Cys
             55                  60                  65
GAG GAC GCC GCA CGC GAG CTG CAG AGC CAG ATA CAG GAG GCC CGA GCC        295
Glu Asp Ala Ala Arg Glu Leu Gln Ser Gln Ile Gln Glu Ala Arg Ala
         70                  75                  80
GAC TTA GCC CGC AGG GGG CTG CGC TTC TGACAGCCTA ACCCCATT                340
Asp Leu Ala Arg Arg Gly Leu Arg Phe
     85                  90
CCTGTGCGGA CAGCCCTTCC TCCCATTTCC CATTAAAGAG CCAGTTTATT TTCT            394
```

Sequence No.: 60
Sequence length: 732
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Lymphoma

Cell line: U937
Clone name: HP10076
Sequence characteristics
Code representing characteristics: CDS
Existence site: 82.. 600
Characterization method: E
Sequence description

```
AGAAACGTGT TCGCTGCCCA GAAGAAGGGA AGGCGCGAGT GAGGAAAGGA GGTACTGTAG     60
ATGCCCTCCA AATCCTTGGT T ATG GAA TAT TTG GCT CAT CCC AGT ACA CTC      111
                        Met Glu Tyr Leu Ala His Pro Ser Thr Leu
                          1               5                  10
GGC TTG GCT GTT GGA GTT GCT TGT GGC ATG TGC CTG GGC TGG AGC CTT      159
Gly Leu Ala Val Gly Val Ala Cys Gly Met Cys Leu Gly Trp Ser Leu
                 15                  20                  25
CGA GTA TGC TTT GGG ATG CTC CCC AAA AGC AAG ACG AGC AAG ACA CAC      207
Arg Val Cys Phe Gly Met Leu Pro Lys Ser Lys Thr Ser Lys Thr His
             30                  35                  40
ACA GAT ACT GAA AGT GAA GCA AGC ATC TTG GGA GAC AGC GGG GAG TAC      255
Thr Asp Thr Glu Ser Glu Ala Ser Ile Leu Gly Asp Ser Gly Glu Tyr
         45                  50                  55
AAG ATG ATT CTT GTG GTT CGA AAT GAC TTA AAG ATG GGA AAA GGG AAA      303
Lys Met Ile Leu Val Val Arg Asn Asp Leu Lys Met Gly Lys Gly Lys
     60                  65                  70
GTG GCT GCC CAG TGC TCT CAT GCT GCT GTT TCA GCC TAC AAG CAG ATT      351
Val Ala Ala Gln Cys Ser His Ala Ala Val Ser Ala Tyr Lys Gln Ile
 75                  80                  85                  90
CAA AGA AGA AAT CCT GAA ATG CTC AAA CAA TGG GAA TAC TGT GGC CAG      399
Gln Arg Arg Asn Pro Glu Met Leu Lys Gln Trp Glu Tyr Cys Gly Gln
                 95                 100                 105
CCC AAG GTG GTG GTC AAA GCT CCT GAT GAA GAA ACC CTG ATT GCA TTA      447
Pro Lys Val Val Val Lys Ala Pro Asp Glu Glu Thr Leu Ile Ala Leu
            110                 115                 120
TTG GCC CAT GCA AAA ATG CTG GGA CTG ACT GTA AGT TTA ATT CAA GAT      495
Leu Ala His Ala Lys Met Leu Gly Leu Thr Val Ser Leu Ile Gln Asp
        125                 130                 135
GCT GGA CGT ACT CAG ATT GCA CCA GGC TCT CAA ACT GTC CTA GGG ATT      543
Ala Gly Arg Thr Gln Ile Ala Pro Gly Ser Gln Thr Val Leu Gly Ile
    140                 145                 150
GGG CCA GGA CCA GCA GAC CTA ATT GAC AAA GTC ACT GGT CAC CTA AAA      591
Gly Pro Gly Pro Ala Asp Leu Ile Asp Lys Val Thr Gly His Leu Lys
155                 160                 165                 170
CTT TAC TAGGTGGACT TTGATATGAC AACAACCCCT CCATCACAAG TGT              640
Leu Tyr
```

TTGAAGCCTG TCAGATTCTA ACAACAAAAG CTGAATTTCT TCACCCAACT TAAATGTTCT 700
TGAGATGAAA ATAAAACCTA TTCCCATGTT CT 732

Sequence No.: 61
Sequence length: 697
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Lymphoma
  Cell line: U937
  Clone name: HP10085
Sequence characteristics
  Code representing characteristics: CDS
  Existence site: 151.. 600
  Characterization method: E
Sequence description

```
TATACCTCTA GTTTGGAGCT GTGCTGTAAA AACAAGAGTA ACATTTTTAT ATTAAAGTTA    60
AATAAAGTTA CAACTTTGAA GAGAGTTTCT GCAAGACATG ACACAAAGCT GCTAGCAGAA   120
AATCAAAACG CTGATTAAAA GAAGCACGGT ATG ATG ACC AAA CAT AAA AAG TGT    174
                                 Met Met Thr Lys His Lys Lys Cys
                                   1               5
TTT ATA ATT GTT GGT GTT TTA ATA ACA ACT AAT ATT ATT ACT CTG ATA     222
Phe Ile Ile Val Gly Val Leu Ile Thr Thr Asn Ile Ile Thr Leu Ile
     10                  15                  20
GTT AAA CTA ACT CGA GAT TCT CAG AGT TTA TGC CCC TAT GAT TGG ATT     270
Val Lys Leu Thr Arg Asp Ser Gln Ser Leu Cys Pro Tyr Asp Trp Ile
 25                  30                  35                  40
GGT TTC CAA AAC AAA TGC TAT TAT TTC TCT AAA GAA GAA GGA GAT TGG     318
Gly Phe Gln Asn Lys Cys Tyr Tyr Phe Ser Lys Glu Glu Gly Asp Trp
                 45                  50                  55
AAT TCA AGT AAA TAC AAC TGT TCC ACT CAA CAT GCC GAC CTA ACT ATA     366
Asn Ser Ser Lys Tyr Asn Cys Ser Thr Gln His Ala Asp Leu Thr Ile
             60                  65                  70
ATT GAC AAC ATA GAA GAA ATG AAT TTT CTT AGG CGG TAT AAA TGC AGT     414
Ile Asp Asn Ile Glu Glu Met Asn Phe Leu Arg Arg Tyr Lys Cys Ser
         75                  80                  85
TCT GAT CAC TGG ATT GGA CTG AAG ATG GCA AAA AAT CGA ACA GGA CAA     462
Ser Asp His Trp Ile Gly Leu Lys Met Ala Lys Asn Arg Thr Gly Gln
```

90 95 100
TGG GTA GAT GGA GCT ACA TTT ACC AAA TCG TTT GGC ATG AGA GGG AGT 510
Trp Val Asp Gly Ala Thr Phe Thr Lys Ser Phe Gly Met Arg Gly Ser
105 110 115 120
GAA GGA TGT GCC TAC CTC AGC GAT GAT GGT GCA GCA ACA GCT AGA TGT 558
Glu Gly Cys Ala Tyr Leu Ser Asp Asp Gly Ala Ala Thr Ala Arg Cys
125 130 135
TAC ACC GAA AGA AAA TGG ATT TGC AGG AAA AGA ATA CAC TAA 600
Tyr Thr Glu Arg Lys Trp Ile Cys Arg Lys Arg Ile His
140 145
GTTAATGTCT AAGATAATGG GGAAAATAGA AAATAACATT ATTAAGTGTA AAACCAGCAA 660
AGTACTTTTT TAATTAAACA AAGTTCGAGT TTTGTAC 697

Sequence No.: 62
Sequence length: 1186
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
Organism species: *Homo sapiens*
Cell kind: Stomach cancer
Clone name: HP10122
Sequence characteristics
Code representing characteristics: CDS
Existence site: 139.. 705
Characterization method: E
Sequence description

AAGTGCGATC TTCGGGCTGT CAGAGTTGGT CTGTTACTCG GTGGTGGCGG AGTCTACGGA 60
AGCCGTTTTC GCTTCACTTT TCCTGGCTGT AGAGCGCTTT CCCCCTGGCG GGTGAGAGTG 120
CAGAGACGAA GGTGCGAG ATG AGC ACT ATG TTC GCG GAC ACT CTC CTC ATC 171
Met Ser Thr Met Phe Ala Asp Thr Leu Leu Ile
1 5 10
GTT TTT ATC TCT GTG TGC ACG GCT CTG CTC GCA GAG GGC ATA ACC TGG 219
Val Phe Ile Ser Val Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp
15 20 25
GTC CTG GTT TAC AGG ACA GAC AAG TAC AAG AGA CTG AAG GCA GAA GTG 267
Val Leu Val Tyr Arg Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val
30 35 40
GAA AAA CAG AGT AAA AAA TTG GAA AAG AAG AAG GAA ACA ATA ACA GAG 315
Glu Lys Gln Ser Lys Lys Leu Glu Lys Lys Lys Glu Thr Ile Thr Glu
45 50 55

```
TCA GCT GGT CGA CAA CAG AAA AAG AAA ATA GAG AGA CAA GAA GAG AAA      363
Ser Ala Gly Arg Gln Gln Lys Lys Lys Ile Glu Arg Gln Glu Glu Lys
 60                  65                  70                  75
CTG AAG AAT AAC AAC AGA GAT CTA TCA ATG GTT CGA ATG AAA TCC ATG      411
Leu Lys Asn Asn Asn Arg Asp Leu Ser Met Val Arg Met Lys Ser Met
                 80                  85                  90
TTT GCT ATT GGC TTT TGT TTT ACT GCC CTA ATG GGA ATG TTC AAT TCC      459
Phe Ala Ile Gly Phe Cys Phe Thr Ala Leu Met Gly Met Phe Asn Ser
             95                 100                 105
ATA TTT GAT GGT AGA GTG GTG GCA AAG CTT CCT TTT ACC CCT CTT TCT      507
Ile Phe Asp Gly Arg Val Val Ala Lys Leu Pro Phe Thr Pro Leu Ser
        110                 115                 120
TAC ATC CAA GGA CTG TCT CAT CGA AAT CTG CTG GGA GAT GAC ACC ACA      555
Tyr Ile Gln Gly Leu Ser His Arg Asn Leu Leu Gly Asp Asp Thr Thr
    125                 130                 135
GAC TGT TCC TTC ATT TTC CTG TAT ATT CTC TGT ACT ATG TCG ATT CGA      603
Asp Cys Ser Phe Ile Phe Leu Tyr Ile Leu Cys Thr Met Ser Ile Arg
140                 145                 150                 155
CAG AAC ATT CAG AAG ATT CTC GGC CTT GCC CCT TCA CGA GCC GCC ACC      651
Gln Asn Ile Gln Lys Ile Leu Gly Leu Ala Pro Ser Arg Ala Ala Thr
                160                 165                 170
AAG CAG GCA GGT GGA TTT CTT GGC CCA CCA CCT CCT TCT GGG AAG TTC      699
Lys Gln Ala Gly Gly Phe Leu Gly Pro Pro Pro Pro Ser Gly Lys Phe
            175                 180                 185
TCT TGAACTCAAG AACTCTTTAT TTTCTATCAT TCTTTCTAGA CACACACA             750
Ser

CATCAGACTG GCAACTGTTT TGTAGCAAGA GCCATAGGTA GCCTTACTAC TTGGGCCTCT    810
TTCTAGTTTT GAATTATTTC TAAGCCTTTT GGGTATGATT AGAGTGAAAA TGGCAGCCAG    870
CAAACTTGAT AGTGCTTTTG GTCCTAGATG ATTTTTATCA AATAAGTGGA TTGATTAGTT    930
AAGTTCAGGT AATGTTTATG TAATGAAAAA CAAATAGCAT CCTTCTTGTT TCATTTACAT    990
AAGTATTTTC TGTGGGACCG ACTCTCAAGG CACTGTGTAT GCCCTGCAAG TTGGCTGTCT   1050
ATGAGCATTT AGAGATTTAG AAGAAAAATT TAGTTTGTTT AACCCTTGTA ACTGTTTGTT   1110
TTGTTGTTGT TTTTTTTTCA AGCCAAATAC ATGACATAAG ATCAATAAAG AGGCCAAATT   1170
TTTAGCTGTT TTATGT                                                   1186
```

Sequence No.: 63
Sequence length: 1409
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:

Organism species: *Homo sapiens*
Cell kind: Lymphoma
Cell line: U937
Clone name: HP10136

Sequence characteristics
Code representing characteristics: CDS
Existence site: 82.. 729
Characterization method: E

Sequence description

```
ATAACTGTTG TCGCGGCGGA GGAAGTGAGG ACGGCGCCAA GGGCCTTCCG GGCCAGTGTT      60
GGATCCCTGT AGTTTGTGAA G ATG GTG TTG CTA ACA ATG ATC GCC CGA GTG       111
                        Met Val Leu Leu Thr Met Ile Ala Arg Val
                          1               5                  10
GCG GAC GGG CTC CCG CTG GCC GCC TCG ATG CAG GAG GAC GAA CAG TCT       159
Ala Asp Gly Leu Pro Leu Ala Ala Ser Met Gln Glu Asp Glu Gln Ser
                 15                  20                  25
GGC CGG GAC CTT CAA CAG TAT CAG AGT CAG GCT AAG CAA CTC TTT CGA       207
Gly Arg Asp Leu Gln Gln Tyr Gln Ser Gln Ala Lys Gln Leu Phe Arg
             30                  35                  40
AAG TTG AAT GAA CAG TCC CCT ACC AGA TGT ACC TTG GAA GCA GGA GCC       255
Lys Leu Asn Glu Gln Ser Pro Thr Arg Cys Thr Leu Glu Ala Gly Ala
         45                  50                  55
ATG ACT TTT CAC TAC ATT ATT GAG CAG GGG GTG TGT TAT TTG GTT TTA       303
Met Thr Phe His Tyr Ile Ile Glu Gln Gly Val Cys Tyr Leu Val Leu
     60                  65                  70
TGT GAA GCT GCC TTC CCT AAG AAG TTG GCT TTT GCC TAC CTA GAA GAT       351
Cys Glu Ala Ala Phe Pro Lys Lys Leu Ala Phe Ala Tyr Leu Glu Asp
 75                  80                  85                  90
TTG CAC TCA GAA TTT GAT GAA CAG CAT GGA AAG AAG GTG CCC ACT GTG       399
Leu His Ser Glu Phe Asp Glu Gln His Gly Lys Lys Val Pro Thr Val
                 95                 100                 105
TCC CGA CCC TAT TCC TTT ATT GAA TTT GAT ACT TTC ATT CAG AAA ACC       447
Ser Arg Pro Tyr Ser Phe Ile Glu Phe Asp Thr Phe Ile Gln Lys Thr
            110                 115                 120
AAG AAG CTC TAC ATT GAC AGT CGT GCT CGA AGA AAT CTA GGC TCC ATC       495
Lys Lys Leu Tyr Ile Asp Ser Arg Ala Arg Arg Asn Leu Gly Ser Ile
        125                 130                 135
AAC ACT GAA TTG CAA GAT GTG CAG AGG ATC ATG GTG GCC AAT ATT GAA       543
Asn Thr Glu Leu Gln Asp Val Gln Arg Ile Met Val Ala Asn Ile Glu
    140                 145                 150
GAA GTG TTA CAA CGA GGA GAA GCA CTC TCA GCA TTG GAT TCA AAG GCT       591
Glu Val Leu Gln Arg Gly Glu Ala Leu Ser Ala Leu Asp Ser Lys Ala
155                 160                 165                 170
```

```
AAC AAT TTG TCC AGT CTG TCC AAG AAA TAC CGC CAG GAT GCG AAG TAC      639
Asn Asn Leu Ser Ser Leu Ser Lys Lys Tyr Arg Gln Asp Ala Lys Tyr
                175                 180                 185
TTG AAC ATG CGT TCC ACT TAT GCC AAA CTT GCA GCA GTA GCT GTA TTT      687
Leu Asn Met Arg Ser Thr Tyr Ala Lys Leu Ala Ala Val Ala Val Phe
            190                 195                 200
TTC ATC ATG TTA ATA GTG TAT GTC CGA TTC TGG TGG CTG TGAA             730
Phe Ile Met Leu Ile Val Tyr Val Arg Phe Trp Trp Leu
        205                 210                 215
ATAATGAATA CAGTCACTGG TAAGGGAGAA CCTAGAACCC AGTAGGTGTA TATTTTCAGG    790
AAACTGAGCT CACAGAGATG TGTATTAGAA TCCAAGTGGA ACTTCTGCCT CTAAAGACCT    850
TGCAAGAAAA GAGATGCCCT GAAAATGAAA GGTTGCACCT CATTTAATGA AGCTTAACCC    910
TATGTAGAAA GTCTCTTTCG GGGGCAGAGG CTTTCTCTGG GTGCCAAGCC ATATATATTA    970
GGGAATAGTA GATTGTTAAT TTCGTTTTTT CCCTCCCAGT GCATTTTAAA AACAGCACTG   1030
GCTGGGGCAT TCTCATTCTC TGATGGAGCC ATCAATGAGA TTTAACTTAG TCAACCTGTG   1090
CTAGCAACAT TCTGAAATTC CTTCAAAGAA GGCAGTCCTT TGGGAAGGTG TTTTTTTTTT   1150
TTTTTTTTTT TTTGACTCTA ATCAACATTC CTTTTGTTGG TGACATTTGT GATTTTCAGT   1210
AATCTGAGTT TTTGATGGCC TTTTAAACAA GACTCCAGTA TGTGAAGGTT AATTGCTGTG   1270
CTCCACAGAT CTTGTCTATT GGCCCCTGTA GAAAGTTAAC CTTTGTTGTT TTCCTTTTAT   1330
AATTTGCTTA TTGCACAATT GCTTTAGGGT AAGTGAATTA TATTAAGATG CCTTGAAATT   1390
ATAGCACTCC TTGATTAAG                                                1409
```

Sequence No.: 64
Sequence length: 974
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Stomach cancer
  Clone name: HP10175
Sequence characteristics
  Code representing characteristics: CDS
  Existence site: 174.. 512
  Characterization method: E
Sequence description

```
AGAGCCGCTC CCCTCTCCTC GCCCCGCCAC CGGGACGGAG AGCGCCCGCC GCTGCATTTC      60
CGGCGACACC TCGCAGTCAT TCCTGCGGCT TGCGCGCCCT TGTAGACAGC CGGGGCCTTC     120
GTGAGACCGG TGCAGGCCTG GGTAGTCTCC CTGTCTGGAC AGAGAAGAGA AAA ATG       176
                                                           Met
                                                             1
```

```
CAG GAC ACT GGC TCA GTA GTG CCT TTG CAT TGG TTT GGC TTT GGC TAC       224
Gln Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly Phe Gly Tyr
                5                  10                  15
GCA GCA CTG GTT GCT TCT GGT GGG ATC ATT GGC TAT GTA AAA GCA GGC       272
Ala Ala Leu Val Ala Ser Gly Gly Ile Ile Gly Tyr Val Lys Ala Gly
         20                  25                  30
AGC GTG CCG TCC CTG GCT GCA GGG CTG CTC TTT GGC AGT CTA GCC GGC       320
Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu Ala Gly
     35                  40                  45
CTG GGT GCT TAC CAG CTG TCT CAG GAT CCA AGG AAC GTT TGG GTT TTC       368
Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val Trp Val Phe
 50                  55                  60                  65
CTA GCT ACA TCT GGT ACC TTG GCT GGC ATT ATG GGA ATG AGG TTC TAC       416
Leu Ala Thr Ser Gly Thr Leu Ala Gly Ile Met Gly Met Arg Phe Tyr
                 70                  75                  80
CAC TCT GGA AAA TTC ATG CCT GCA GGT TTA ATT GCA GGT GCC AGT TTG       464
His Ser Gly Lys Phe Met Pro Ala Gly Leu Ile Ala Gly Ala Ser Leu
                85                  90                  95
CTG ATG GTC GCC AAA GTT GGA GTT AGT ATG TTC AAC AGA CCC CAT           509
Leu Met Val Ala Lys Val Gly Val Ser Met Phe Asn Arg Pro His
        100                 105                 110
T AGCAGAAGTC ATGTTCCAGC TTAGACTGAT GAAGAATTAA AAATCTGCAT              560
CTTCCACTAT TTTCAATATA TTAAGAGAAA TAAGTGCAGC ATTTTTGCAT CTGACATTTT     620
ACCTAAAAAA AAAGACACCA AACTTGGCAG AGAGGTGGAA AATCAGTCAT GATTACAAAC     680
CTACAGAGGT GGCGAGTATG TAACACAAGA GCTTAATAAG ACCCTCATAG AGCTTGATTC     740
TTGTATATTG ATGTTGTCTT TTCTTTCTGT ATCTGTAGGT AAATCTCAAG GGTAAAATGT     800
TAGGTGTCAG CTTTCAGGGC TCTGAAACCC TATTCCCTGC TCTGAGGAAC AGTGTGAAAA     860
AAAGTCTTTT AGGAGATTTA CAATATCTGT TCTTTTGCTC ATCTTAGACC ACAGACTGAC     920
TTTGAAATTA TGTTAAGTGA AATATCAATG TAAATAAAGT TTACTATAAA TAAT           974
```

Sequence No.: 65
Sequence length: 925
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Epidermoid carcinoma
  Cell line: KB
  Clone name: HP10179
Sequence characteristics
  Code representing characteristics: CDS

Existence site: 122.. 466
Characterization method: E
Sequence description

```
AATCGCGTTT CCGGAGAGAC CTGGCTGCTG TGTCCCGCGG CTTGCGCTCC GTAGTGGACT     60
CCGCGGGCCT TCGGCAGATG CAGGCCTGGG GTAGTCTCCT TTCTGGACTG AGAAGAGAAG    120
ATG GAG AAG CCC CTC TTC CCA TTA GTG CCT TTG CAT TGG TTT GGC TTT      168
Met Glu Lys Pro Leu Phe Pro Leu Val Pro Leu His Trp Phe Gly Phe
 1               5                  10                  15
GGC TAC ACA GCA CTG GTT GTT TCT GGT GGG ATC GTT GGC TAT GTA AAA      216
Gly Tyr Thr Ala Leu Val Val Ser Gly Gly Ile Val Gly Tyr Val Lys
            20                  25                  30
ACA GGC AGC GTG CCG TCC CTG GCA GCA GGG CTG CTC TTC GGC AGT CTA      264
Thr Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu
        35                  40                  45
GCC GGC CTG GGT GCT TAC CAG CTG TAT CAG GAT CCT AGG AAC GTT TGG      312
Ala Gly Leu Gly Ala Tyr Gln Leu Tyr Gln Asp Pro Arg Asn Val Trp
    50                  55                  60
GGT TTC CTA GCC GCT ACA TCT GTT ACT TTT GTT GGT GTT ATG GGA ATA      360
Gly Phe Leu Ala Ala Thr Ser Val Thr Phe Val Gly Val Met Gly Met
65                  70                  75                  80
AGA TCC TAC TAC TAT GGA AAA TTC ATG CCT GTA GGT TTA ATT GCA GGT      408
Arg Ser Tyr Tyr Tyr Gly Lys Phe Met Pro Val Gly Leu Ile Ala Gly
                85                  90                  95
GCC AGT TTG CTG ATG GCC GCC AAA GTT GGA GTT CGT ATG TTG ATG ACA      456
Ala Ser Leu Leu Met Ala Ala Lys Val Gly Val Arg Met Leu Met Thr
            100                 105                 110
TCT GAT TAGCAGAAGT CATGTTCGCA GCTTGGACTC ATGAAGGATT AAAAATCT         510
Ser Asp

GCATCTTCCA CTATTTTCAA TGTATTAAGA GAAATAAGTG CAGCATTTTT GCATCTGACA    570
TTTTACCTAA AAAAAAAAAG ACACCAAATT TGGCGGAGGG GTGGAAAATC AGTTGTTACC    630
ATTATAACCC TACAGAGGTG GTGAGCATGT AACATGAGCT TATTGAGACC ATCATAGAGA    690
TCGATTCTTG TATATTGATT TTATCTCTTT CTGTATCTAT AGGTAAATCT CAAGGGTAAA    750
ATGTTAGGTG TTGACATTGA GAACCCTGAA ACCCCATTCC CTGCTCAGAG GAACAGTGTG    810
AAAAAAAATC TCTTGAGAGA TTTAGAATAT CTTTTCTTTT GCTCATCTTA GACCACAGAC    870
TGACTTTGAA ATTATGTTAA GTGAAATATC AATGAAAATA AAGTTTACTA TAAAT         925
```

Sequence No.: 66
Sequence length: 1115
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear

Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Fibrosarcoma
  Cell line: HT-1080
  Clone name: HP10196
Sequence characteristics
  Code representing characteristics: CDS
  Existence site: 10.. 993
  Characterization method: E
Sequence description

```
GCGGGGAAA ATG GCG GCG GCG GCG GCG GCG GCT GCA GCT ACG AAC GGG ACC      51
          Met Ala Ala Ala Ala Ala Ala Ala Ala Ala Thr Asn Gly Thr
            1               5                   10
GGA GGA AGC AGC GGG ATG GAG GTG GAT GCA GCA GTA GTC CCC AGC GTG        99
Gly Gly Ser Ser Gly Met Glu Val Asp Ala Ala Val Val Pro Ser Val
 15                  20                  25                  30
ATG GCC TGC GGA GTG ACT GGG AGT GTT TCC GTC GCT CTC CAT CCC CTT       147
Met Ala Cys Gly Val Thr Gly Ser Val Ser Val Ala Leu His Pro Leu
                 35                  40                  45
GTC ATT CTC AAC ATC TCA GAC CAC TGG ATC CGC ATG CGC TCC CAG GAG       195
Val Ile Leu Asn Ile Ser Asp His Trp Ile Arg Met Arg Ser Gln Glu
             50                  55                  60
GGG CGG CCT GTG CAG GTG ATT GGG GCT CTG ATT GGC AAG CAG GAG GGC       243
Gly Arg Pro Val Gln Val Ile Gly Ala Leu Ile Gly Lys Gln Glu Gly
         65                  70                  75
CGA AAT ATC GAG GTG ATG AAC TCC TTT GAG CTG CTG TCC CAC ACC GTG       291
Arg Asn Ile Glu Val Met Asn Ser Phe Glu Leu Leu Ser His Thr Val
     80                  85                  90
GAA GAG AAG ATT ATC ATT GAC AAG GAA TAT TAT TAC ACC AAG GAG GAG       339
Glu Glu Lys Ile Ile Ile Asp Lys Glu Tyr Tyr Tyr Thr Lys Glu Glu
 95                 100                 105                 110
CAG TTT AAA CAG GTG TTC AAG GAG CTG GAG TTT CTG GGT TGG TAT ACC       387
Gln Phe Lys Gln Val Phe Lys Glu Leu Glu Phe Leu Gly Trp Tyr Thr
                115                 120                 125
ACA GGG GGG CCA CCT GAC CCC TCG GAC ATC CAC GTC CAT AAG CAG GTG       435
Thr Gly Gly Pro Pro Asp Pro Ser Asp Ile His Val His Lys Gln Val
            130                 135                 140
TGT GAG ATC ATC GAG AGC CCC CTC TTT CTG AAG TTG AAC CCT ATG ACC       483
Cys Glu Ile Ile Glu Ser Pro Leu Phe Leu Lys Leu Asn Pro Met Thr
        145                 150                 155
AAG CAC ACA GAT CTT CCT GTC AGC GTT TTT GAG TCT GTC ATT GAT ATA       531
Lys His Thr Asp Leu Pro Val Ser Val Phe Glu Ser Val Ile Asp Ile
```

```
    160                 165                 170
ATC AAT GGA GAG GCC ACA ATG CTG TTT GCT GAG CTG ACC TAC ACT CTG      579
Ile Asn Gly Glu Ala Thr Met Leu Phe Ala Glu Leu Thr Tyr Thr Leu
175                 180                 185                 190
GCC ACA GAG GAA GCG GAA CGC ATT GGT GTA GAC CAC GTA GCC CGA ATG      627
Ala Thr Glu Glu Ala Glu Arg Ile Gly Val Asp His Val Ala Arg Met
                195                 200                 205
ACA GCA ACA GGC AGT GGA GAG AAC TCC ACT GTG GCT GAA CAC CTG ATA      675
Thr Ala Thr Gly Ser Gly Glu Asn Ser Thr Val Ala Glu His Leu Ile
            210                 215                 220
GCA CAG CAC AGC GCC ATC AAG ATG CTG CAC AGC CGC GTC AAG CTC ATC      723
Ala Gln His Ser Ala Ile Lys Met Leu His Ser Arg Val Lys Leu Ile
        225                 230                 235
TTG GAG TAC GTC AAG GCC TCT GAA GCG GGA GAG GTC CCC TTT AAT CAT      771
Leu Glu Tyr Val Lys Ala Ser Glu Ala Gly Glu Val Pro Phe Asn His
    240                 245                 250
GAG ATC CTG CGG GAG GCC TAT GCT CTG TGT CAC TGT CTC CCG GTG CTC      819
Glu Ile Leu Arg Glu Ala Tyr Ala Leu Cys His Cys Leu Pro Val Leu
255                 260                 265                 270
AGC ACA GAC AAG TTC AAG ACA GAT TTT TAT GAT CAA TGC AAC GAC GTG      867
Ser Thr Asp Lys Phe Lys Thr Asp Phe Tyr Asp Gln Cys Asn Asp Val
                275                 280                 285
GGG CTC ATG GCC TAC CTC GGC ACC ATC ACC AAA ACG TGC AAC ACC ATG      915
Gly Leu Met Ala Tyr Leu Gly Thr Ile Thr Lys Thr Cys Asn Thr Met
            290                 295                 300
AAC CAG TTT GTG AAC AAG TTC AAT GTC CTC TAC GAC CGA CAA GGC ATC      963
Asn Gln Phe Val Asn Lys Phe Asn Val Leu Tyr Asp Arg Gln Gly Ile
        305                 310                 315
GGC AGG AGA ATG CGC GGG CTC TTT TTC TGATGAGGGT                      1000
Gly Arg Arg Met Arg Gly Leu Phe Phe
    320                 325
ACTTGAAGGG CTGATGGACA GGGGTCAGGC AACTATCCCA AAGGGGAGGG CACTACACTT   1060
CCTTGAGAGA AACCACTGTC ATTAATAAAA GGGGAGCAGC CCCTGAGCAC CCCTG        1115
```

Sequence No.: 67
Sequence length: 1721
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Fibrosarcoma

Cell line: HT-1080
Clone name: HP10235
Sequence characteristics
Code representing characteristics: CDS
Existence site: 6.. 1127
Characterization method: E
Sequence description

```
ATGTC ATG ACC CTA TGT GCC ATG CTG CCC CTG CTG TTA TTC ACC TAC CTC      50
      Met Thr Leu Cys Ala Met Leu Pro Leu Leu Leu Phe Thr Tyr Leu
        1               5                  10                  15
AAC TCC TTC CTG CAT CAG AGG ATC CCC CAG TCC GTA CGG ATC CTG GGC        98
Asn Ser Phe Leu His Gln Arg Ile Pro Gln Ser Val Arg Ile Leu Gly
                20                  25                  30
AGC CTG GTG GCC ATC CTG CTG GTG TTT CTG ATC ACT GCC ATC CTG GTG       146
Ser Leu Val Ala Ile Leu Leu Val Phe Leu Ile Thr Ala Ile Leu Val
            35                  40                  45
AAG GTG CAG CTG GAT GCT CTG CCC TTC TTT GTC ATC ACC ATG ATC AAG       194
Lys Val Gln Leu Asp Ala Leu Pro Phe Phe Val Ile Thr Met Ile Lys
        50                  55                  60
ATC GTG CTC ATT AAT TCA TTT GGT GCC ATC CTG CAG GGC AGC CTG TTT       242
Ile Val Leu Ile Asn Ser Phe Gly Ala Ile Leu Gln Gly Ser Leu Phe
    65                  70                  75
GGT CTG GCT GGC CTT CTG CCT GCC AGC TAC ACG GCC CCC ATC ATG AGT       290
Gly Leu Ala Gly Leu Leu Pro Ala Ser Tyr Thr Ala Pro Ile Met Ser
80                  85                  90                  95
GGC CAG GGC CTA GCA GGC TTC TTT GCC TCC GTG GCC ATG ATC TGC GCT       338
Gly Gln Gly Leu Ala Gly Phe Phe Ala Ser Val Ala Met Ile Cys Ala
                100                 105                 110
ATT GCC AGT GGC TCG GAG CTA TCA GAA AGT GCC TTC GGC TAC TTT ATC       386
Ile Ala Ser Gly Ser Glu Leu Ser Glu Ser Ala Phe Gly Tyr Phe Ile
            115                 120                 125
ACA GCC TGT GCT GTT ATC ATT TTG ACC ATC ATC TGT TAC CTG GGC CTG       434
Thr Ala Cys Ala Val Ile Ile Leu Thr Ile Ile Cys Tyr Leu Gly Leu
        130                 135                 140
CCC CGC CTG GAA TTC TAC CGC TAC TAC CAG CAG CTC AAG CTT GAA GGA       482
Pro Arg Leu Glu Phe Tyr Arg Tyr Tyr Gln Gln Leu Lys Leu Glu Gly
    145                 150                 155
CCC GGG GAG CAG GAG ACC AAG TTG GAC CTC ATT AGC AAA GGA GAG GAG       530
Pro Gly Glu Gln Glu Thr Lys Leu Asp Leu Ile Ser Lys Gly Glu Glu
160                 165                 170                 175
CCA AGA GCA GGC AAA GAG GAA TCT GGA GTT TCA GTC TCC AAC TCT CAG       578
Pro Arg Ala Gly Lys Glu Glu Ser Gly Val Ser Val Ser Asn Ser Gln
                180                 185                 190
```

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CCC ACC AAT GAA AGC CAC TCT ATC AAA GCC ATC CTG AAA AAT ATC TCA      626
Pro Thr Asn Glu Ser His Ser Ile Lys Ala Ile Leu Lys Asn Ile Ser
            195                 200                 205
GTC CTG GCT TTC TCT GTC TGC TTC ATC TTC ACT ATC ACC ATT GGG ATG      674
Val Leu Ala Phe Ser Val Cys Phe Ile Phe Thr Ile Thr Ile Gly Met
        210                 215                 220
TTT CCA GCC GTG ACT GTT GAG GTC AAG TCC AGC ATC GCA GGC AGC AGC      722
Phe Pro Ala Val Thr Val Glu Val Lys Ser Ser Ile Ala Gly Ser Ser
    225                 230                 235
ACC TGG GAA CGT TAC TTC ATT CCT GTG TCC TGT TTC TTG ACT TTC AAT      770
Thr Trp Glu Arg Tyr Phe Ile Pro Val Ser Cys Phe Leu Thr Phe Asn
240                 245                 250                 255
ATC TTT GAC TGG TTG GGC CGG AGC CTC ACA GCT GTA TTC ATG TGG CCT      818
Ile Phe Asp Trp Leu Gly Arg Ser Leu Thr Ala Val Phe Met Trp Pro
                260                 265                 270
GGG AAG GAC AGC CGC TGG CTG CCA AGC CTG GTG CTG GCC CGG CTG GTG      866
Gly Lys Asp Ser Arg Trp Leu Pro Ser Leu Val Leu Ala Arg Leu Val
            275                 280                 285
TTT GTG CCA CTG CTG CTG CTG TGC AAC ATT AAG CCC CGC CGC TAC CTG      914
Phe Val Pro Leu Leu Leu Leu Cys Asn Ile Lys Pro Arg Arg Tyr Leu
        290                 295                 300
ACT GTG GTC TTC GAG CAC GAT GCC TGG TTC ATC TTC TTC ATG GCT GCC      962
Thr Val Val Phe Glu His Asp Ala Trp Phe Ile Phe Phe Met Ala Ala
    305                 310                 315
TTT GCC TTC TCC AAC GGC TAC CTC GCC AGC CTC TGC ATG TGC TTC GGG     1010
Phe Ala Phe Ser Asn Gly Tyr Leu Ala Ser Leu Cys Met Cys Phe Gly
320                 325                 330                 335
CCC AAG AAA GTG AAG CCA GCT GAG GCA GAG ACC GCA GGA GCC ATC ATG     1058
Pro Lys Lys Val Lys Pro Ala Glu Ala Glu Thr Ala Gly Ala Ile Met
                340                 345                 350
GCC TTC TTC CTG TGT CTG GGT CTG GCA CTG GGG GCT GTT TTC TCC TTC     1106
Ala Phe Phe Leu Cys Leu Gly Leu Ala Leu Gly Ala Val Phe Ser Phe
            355                 360                 365
CTG TTC CGG GCA ATT GTG TGACAAAGGA TGGACAGAAG GACTGC                1150
Leu Phe Arg Ala Ile Val
        370
CTGCCTCCCT CCCTGTCTGC CTCCTGCCCC TTCCTTCTGC CAGGGGTGAT CCTGAGTGGT   1210
CTGGCGGTTT TTTCTTCTAA CTGACTTCTG CTTTCCACGG CGTGTGCTGG GCCCGGATCT   1270
CCAGGCCCTG GGGAGGGAGC CTCTGGACGG ACAGTGGGGA CATTGTGGGT TTGGGGCTCA   1330
GAGTCGAGGG ACGGGGTGTA GCCTCGGCAT TTGCTTGAGT TTCTCCACTC TTGGCTCTGA   1390
CTGATCCCTG CTTGTGCAGG CCAGTGGAGG CTCTTGGGCT TGGAGAACAC GTGTGTCTCT   1450
GTGTATGTGT CTGTGTGTCT GCGTCCGTGT CTGTCAGACT GTCTGCCTGT CCTGGGGTGG   1510
CTAGGAGCTG GGTCTGACCG TTGTATGGTT TGACCTGATA TACTCCATTC TCCCCTGCGC   1570
CTCCTCCTCT GTGTTCTCTC CATGTCCCCC TCCCAACTCC CCATGCCCAG TTCTTACCCA   1630
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TCATGCACCC TGTACAGTTG CCACGTTACT GCCTTTTTTA AAAATATATT TGACAGAAAC 1690
CAGGTGCCTT CAGAGGCTCT CTGATTTAAA T 1721

Sequence No.: 68
Sequence length: 1504
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Stomach cancer
  Clone name: HP10297
Sequence characteristics
  Code representing characteristics: CDS
  Existence site: 63.. 614
  Characterization method: E
Sequence description

```
CTTTTGCGGC TGCAGCGGGC TTGTAGGTGT CCGGCTTTGC TGGCCCAGCA AGCCTGATAA   60
GC ATG AAG CTC TTA TCT TTG GTG GCT GTG GTC GGG TGT TTG CTG GTG     107
   Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val
    1               5                  10                  15
CCC CCA GCT GAA GCC AAC AAG AGT TCT GAA GAT ATC CGG TGC AAA TGC    155
Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys
                20                  25                  30
ATC TGT CCA CCT TAT AGA AAC ATC AGT GGG CAC ATT TAC AAC CAG AAT    203
Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn
            35                  40                  45
GTA TCC CAG AAG GAC TGC AAC TGC CTG CAC GTG GTG GAG CCC ATG CCA    251
Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro
        50                  55                  60
GTG CCT GGC CAT GAC GTG GAG GCC TAC TGC CTG CTG TGC GAG TGC AGG    299
Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg
    65                  70                  75
TAC GAG GAG CGC AGC ACC ACC ACC ATC AAG GTC ATC ATT GTC ATC TAC    347
Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr
80                  85                  90                  95
CTG TCC GTG GTG GGT GCC CTG TTG CTC TAC ATG GCC TTC CTG ATG CTG    395
Leu Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu
                100                 105                 110
GTG GAC CCT CTG ATC CGA AAG CCG GAT GCA TAC ACT GAG CAA CTG CAC    443
Val Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His
```

```
            115                 120                 125
AAT GAG GAG GAG AAT GAG GAT GCT CGC TCT ATG GCA GCA GCT GCT GCA     491
Asn Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala
        130                 135                 140
TCC CTC GGG GGA CCC CGA GCA AAC ACA GTC CTG GAG CGT GTG GAA GGT     539
Ser Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly
    145                 150                 155
GCC CAG CAG CGG TGG AAG CTG CAG GTG CAG GAG CAG CGG AAG ACA GTC     587
Ala Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val
160                 165                 170                 175
TTC GAT CGG CAC AAG ATG CTC AGC TAGATGGGCT GGTGTGGTTG GGTCAAGGC     640
Phe Asp Arg His Lys Met Leu Ser
                180
CCCAACACCA TGGCTGCCAG CTTCCAGGCT GGACAAAGCA GGGGGCTACT TCTCCCTTCC     700
CTCGGTTCCA GTCTTCCCTT TAAAAGCCTG TGGCATTTTT CCTCCTTCTC CCTAACTTTA     760
GAAATGTTGT ACTTGGCTAT TTTGATTAGG GAAGAGGGAT GTGGTCTCTG ATCTCTGTTG     820
TCTTCTTGGG TCTTTGGGGT TGAAGGGAGG GGGAAGGCAG GCCAGAAGGG AATGGAGACA     880
TTCGAGGCGG CCTCAGGAGT GGATGCGATC TGTCTCTCCT GGCTCCACTC TTGCCGCCTT     940
CCAGCTCTGA GTCTTGGGAA TGTTGTTACC CTTGGAAGAT AAAGCTGGGT CTTCAGGAAC    1000
TCAGTGTCTG GGAGGAAAGC ATGGCCCAGC ATTCAGCATG TGTTCCTTTC TGCAGTGGTT    1060
CTTATCACCA CCTCCCTCCC AGCCCCAGCG CCTCAGCCCC AGCCCCAGCT CCAGCCCTGA    1120
GGACAGCTCT GATGGGAGAG CTGGGCCCCC TGAGCCCACT GGGTCTTCAG GGTGCACTGG    1180
AAGCTGGTGT TCGCTGTCCC CTGTGCACTT CTCGCACTGG GGCATGGAGT GCCCATGCAT    1240
ACTCTGCTGC CGGTCCCCTC ACCTGCACTT GAGGGGTCTG GGCAGTCCCT CCTCTCCCCA    1300
GTGTCCACAG TCACTGAGCC AGACGGTCGG TTGGAACATG AGACTCGAGG CTGAGCGTGG    1360
ATCTGAACAC CACAGCCCCT GTACTTGGGT TGCCTCTTGT CCCTGAACTT CGTTGTACCA    1420
GTGCATGGAG AGAAAATTTT GTCCTCTTGT CTTAGAGTTG TGTGTAAATC AAGGAAGCCA    1480
TCATTAAATT GTTTTATTTC TCTC                                          1504
```

Sequence No.: 69
Sequence length: 532
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Stomach cancer
  Clone name: HP10299
Sequence characteristics
  Code representing characteristics: CDS
  Existence site: 93.. 443
  Characterization method: E

Sequence description

```
GCTCTCTGGT AAAGGCGTGC AGGTGTTGGC CGCGGCCTCT GAGCTGGGAT GAGCCGTGCT    60
CCCGGTGGAA GCAAGGGAGC CCAGCCGGAG CC ATG GCC AGT ACA GTG GTA GCA     113
                                    Met Ala Ser Thr Val Val Ala
                                     1               5
GTT GGA CTG ACC ATT GCT GCT GCA GGA TTT GCA GGC CGT TAC GTT TTG     161
Val Gly Leu Thr Ile Ala Ala Ala Gly Phe Ala Gly Arg Tyr Val Leu
        10                  15                  20
CAA GCC ATG AAG CAT ATG GAG CCT CAA GTA AAA CAA GTT TTT CAA AGC     209
Gln Ala Met Lys His Met Glu Pro Gln Val Lys Gln Val Phe Gln Ser
    25                  30                  35
CTA CCA AAA TCT GCC TTC AGT GGT GGC TAT TAT AGA GGT GGG TTT GAA     257
Leu Pro Lys Ser Ala Phe Ser Gly Gly Tyr Tyr Arg Gly Gly Phe Glu
 40                  45                  50                  55
CCC AAA ATG ACA AAA CGG GAA GCA GCA TTA ATA CTA GGT GTA AGC CCT     305
Pro Lys Met Thr Lys Arg Glu Ala Ala Leu Ile Leu Gly Val Ser Pro
                 60                  65                  70
ACT GCC AAT AAA GGG AAA ATA AGA GAT GCT CAT CGA CGA ATT ATG CTT     353
Thr Ala Asn Lys Gly Lys Ile Arg Asp Ala His Arg Arg Ile Met Leu
             75                  80                  85
TTA AAT CAT CCT GAC AAA GGA GGA TCT CCT TAT ATA GCA GCC AAA ATC     401
Leu Asn His Pro Asp Lys Gly Gly Ser Pro Tyr Ile Ala Ala Lys Ile
        90                  95                 100
AAT GAA GCT AAA GAT TTA CTA GAA GGT CAA GCT AAA AAA TGAAGTAAAT      450
Asn Glu Ala Lys Asp Leu Leu Glu Gly Gln Ala Lys Lys
    105                 110                 115
GTATGATGAA TTTTAAGTTC GTATTAGTTT ATGTATATGA GTACTAAGTT TTTATAATAA    510
AATGCCTCAG AGCTACAATT TT                                             532
```

Sequence No.: 70
Sequence length: 662
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Epidermoid carcinoma
  Cell line: KB
  Clone name: HP10301
Sequence characteristics

Code representing characteristics: CDS
Existence site: 92.. 550
Characterization method: E
Sequence description

```
TCTAGCCCCG CCCCAGGCGA GGGCGCCGCA CCCACACCGC GCTGCGCAGT TTTGTTCTGC      60
TCCAGCTGTT CGAAGGTGAT CCAGACGCAA G ATG GCT GTC CTC TCT AAG GAA       112
                                   Met Ala Val Leu Ser Lys Glu
                                     1               5
TAT GGT TTT GTG CTT CTA ACT GGT GCT GCC AGC TTT ATA ATG GTG GCC      160
Tyr Gly Phe Val Leu Leu Thr Gly Ala Ala Ser Phe Ile Met Val Ala
         10                  15                  20
CAC CTA GCC ATC AAT GTT TCC AAG GCC CGC AAG AAG TAC AAA GTG GAG      208
His Leu Ala Ile Asn Val Ser Lys Ala Arg Lys Lys Tyr Lys Val Glu
     25                  30                  35
TAT CCT ATC ATG TAC AGC ACG GAC CCT GAA AAT GGG CAC ATC TTC AAC      256
Tyr Pro Ile Met Tyr Ser Thr Asp Pro Glu Asn Gly His Ile Phe Asn
 40                  45                  50                  55
TGC ATT CAG CGA GCC CAC CAG AAC ACG TTG GAA GTG TAT CCT CCC TTC      304
Cys Ile Gln Arg Ala His Gln Asn Thr Leu Glu Val Tyr Pro Pro Phe
                 60                  65                  70
TTA TTT TTT CTA GCT GTT GGA GGT GTT TAC CAC CCG CGT ATA GCT TCT      352
Leu Phe Phe Leu Ala Val Gly Gly Val Tyr His Pro Arg Ile Ala Ser
             75                  80                  85
GGC CTG GGC TTG GCC TGG ATT GTT GGA CGA GTT CTT TAT GCT TAT GGC      400
Gly Leu Gly Leu Ala Trp Ile Val Gly Arg Val Leu Tyr Ala Tyr Gly
         90                  95                 100
TAT TAC ACG GGA GAA CCC AGC AAG CGT AGT CGA GGA GCC CTG GGG TCC      448
Tyr Tyr Thr Gly Glu Pro Ser Lys Arg Ser Arg Gly Ala Leu Gly Ser
    105                 110                 115
ATC GCC CTC CTG GGC TTG GTG GGC ACA ACT GTG TGC TCT GCT TTC CAG      496
Ile Ala Leu Leu Gly Leu Val Gly Thr Thr Val Cys Ser Ala Phe Gln
120                 125                 130                 135
CAT CTT GGT TGG GTT AAA AGT GGC TTG GGC AGT GGA CCC AAA TGC TGC      544
His Leu Gly Trp Val Lys Ser Gly Leu Gly Ser Gly Pro Lys Cys Cys
                140                 145                 150
CAT TAAAGAATTA TAGGGGTTTA AAAACTCTCA TTCATTTTAA ATG                  590
His

ACTTACCTTT ATTTCCAGTT ACATTTTTTT TCTAAATATA ATAAAAACTT ACCTGGCATC      650
AGCCTCATAC CT                                                        662
```

Sequence No.: 71

Sequence length: 2373
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Liver
  Clone name: HP10302
Sequence characteristics
  Code representing characteristics: CDS
  Existence site: 134.. 1813
  Characterization method: E
Sequence description

```
GAAGACCCCA GCGCCGGCGC GGCTCAGGGC TGGGCCCACG GGACTCCGGA CGCGCCGCGA     60
AAGCGTTGCG CTCCCGGAGG CGTCCGCAGC TGCTGGCTGC TCATTTGCCG GTGACCGGAG    120
GCTCGGGGCC AGC ATG GCC CCC ACG CTG CAA CAG GCG TAC CGG AGG CGC       169
               Met Ala Pro Thr Leu Gln Gln Ala Tyr Arg Arg Arg
                 1               5                  10
TGG TGG ATG GCC TGC ACG GCT GTG CTG GAG AAC CTC TTC TTC TCT GCT      217
Trp Trp Met Ala Cys Thr Ala Val Leu Glu Asn Leu Phe Phe Ser Ala
        15                  20                  25
GTA CTC CTG GGC TGG GGC TCC CTG TTG ATC ATT CTG AAG AAC GAG GGC      265
Val Leu Leu Gly Trp Gly Ser Leu Leu Ile Ile Leu Lys Asn Glu Gly
    30                  35                  40
TTC TAT TCC AGC ACG TGC CCA GCT GAG AGC AGC ACC AAC ACC ACC CAG      313
Phe Tyr Ser Ser Thr Cys Pro Ala Glu Ser Ser Thr Asn Thr Thr Gln
 45                  50                  55                  60
GAT GAG CAG CGC AGG TGG CCA GGC TGT GAC CAG CAG GAC GAG ATG CTC      361
Asp Glu Gln Arg Arg Trp Pro Gly Cys Asp Gln Gln Asp Glu Met Leu
                 65                  70                  75
AAC CTG GGC TTC ACC ATT GGT TCC TTC GTG CTC AGC GCC ACC ACC CTG      409
Asn Leu Gly Phe Thr Ile Gly Ser Phe Val Leu Ser Ala Thr Thr Leu
             80                  85                  90
CCA CTG GGG ATC CTC ATG GAC CGC TTT GGC CCC CGA CCC GTG CGG CTG      457
Pro Leu Gly Ile Leu Met Asp Arg Phe Gly Pro Arg Pro Val Arg Leu
        95                 100                 105
GTT GGC AGT GCC TGC TTC ACT GCG TCC TGC ACC CTC ATG GCC CTG GCC      505
Val Gly Ser Ala Cys Phe Thr Ala Ser Cys Thr Leu Met Ala Leu Ala
    110                 115                 120
TCC CGG GAC GTG GAA GCT CTG TCT CCG TTG ATA TTC CTG GCG CTG TCC      553
Ser Arg Asp Val Glu Ala Leu Ser Pro Leu Ile Phe Leu Ala Leu Ser
125                 130                 135                 140
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CTG AAT GGC TTT GGT GGC ATC TGC CTA ACG TTC ACT TCA CTC ACG CTG 601
Leu Asn Gly Phe Gly Gly Ile Cys Leu Thr Phe Thr Ser Leu Thr Leu
145 150 155

CCC AAC ATG TTT GGG AAC CTG CGC TCC ACG TTA ATG GCC CTC ATG ATT 649
Pro Asn Met Phe Gly Asn Leu Arg Ser Thr Leu Met Ala Leu Met Ile
160 165 170

GGC TCT TAC GCC TCT TCT GCC ATT ACG TTC CCA GGA ATC AAG CTG ATC 697
Gly Ser Tyr Ala Ser Ser Ala Ile Thr Phe Pro Gly Ile Lys Leu Ile
175 180 185

TAC GAT GCC GGT GTG GCC TTC GTG GTC ATC ATG TTC ACC TGG TCT GGC 745
Tyr Asp Ala Gly Val Ala Phe Val Val Ile Met Phe Thr Trp Ser Gly
190 195 200

CTG GCC TGC CTT ATC TTT CTG AAC TGC ACC CTC AAC TGG CCC ATC GAA 793
Leu Ala Cys Leu Ile Phe Leu Asn Cys Thr Leu Asn Trp Pro Ile Glu
205 210 215 220

GCC TTT CCT GCC CCT GAG GAA GTC AAT TAC ACG AAG AAG ATC AAG CTG 841
Ala Phe Pro Ala Pro Glu Glu Val Asn Tyr Thr Lys Lys Ile Lys Leu
225 230 235

AGT GGG CTG GCC CTG GAC CAC AAG GTG ACA GGT GAC CTC TTC TAC ACC 889
Ser Gly Leu Ala Leu Asp His Lys Val Thr Gly Asp Leu Phe Tyr Thr
240 245 250

CAT GTG ACC ACC ATG GGC CAG AGG CTC AGC CAG AAG GCC CCC AGC CTG 937
His Val Thr Thr Met Gly Gln Arg Leu Ser Gln Lys Ala Pro Ser Leu
255 260 265

GAG GAC GGT TCG GAT GCC TTC ATG TCA CCC CAG GAT GTT CGG GGC ACC 985
Glu Asp Gly Ser Asp Ala Phe Met Ser Pro Gln Asp Val Arg Gly Thr
270 275 280

TCA GAA AAC CTT CCT GAG AGG TCT GTC CCC TTA CGC AAG AGC CTC TGC 1033
Ser Glu Asn Leu Pro Glu Arg Ser Val Pro Leu Arg Lys Ser Leu Cys
285 290 295 300

TCC CCC ACT TTC CTG TGG AGC CTC CTC ACC ATG GGC ATG ACC CAG CTG 1081
Ser Pro Thr Phe Leu Trp Ser Leu Leu Thr Met Gly Met Thr Gln Leu
305 310 315

CGG ATC ATC TTC TAC ATG GCT GCT GTG AAC AAG ATG CTG GAG TAC CTT 1129
Arg Ile Ile Phe Tyr Met Ala Ala Val Asn Lys Met Leu Glu Tyr Leu
320 325 330

GTG ACT GGT GGC CAG GAG CAT GAG ACA AAT GAA CAG CAA CAA AAG GTG 1177
Val Thr Gly Gly Gln Glu His Glu Thr Asn Glu Gln Gln Gln Lys Val
335 340 345

GCA GAG ACA GTT GGG TTC TAC TCC TCC GTC TTC GGG GCC ATG CAG CTG 1225
Ala Glu Thr Val Gly Phe Tyr Ser Ser Val Phe Gly Ala Met Gln Leu
350 355 360

TTG TGC CTT CTC ACC TGC CCC CTC ATT GGC TAC ATC ATG GAC TGG CGG 1273
Leu Cys Leu Leu Thr Cys Pro Leu Ile Gly Tyr Ile Met Asp Trp Arg

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365                 370                 375                 380
ATC AAG GAC TGC GTG GAC GCC CCA ACT CAG GGC ACT GTC CTC GGA GAT      1321
Ile Lys Asp Cys Val Asp Ala Pro Thr Gln Gly Thr Val Leu Gly Asp
                385                 390                 395
GCC AGG GAC GGG GTT GCT ACC AAA TCC ATC AGA CCA CGC TAC TGC AAG      1369
Ala Arg Asp Gly Val Ala Thr Lys Ser Ile Arg Pro Arg Tyr Cys Lys
            400                 405                 410
ATC CAA AAG CTC ACC AAT GCC ATC AGT GCC TTC ACC CTG ACC AAC CTG      1417
Ile Gln Lys Leu Thr Asn Ala Ile Ser Ala Phe Thr Leu Thr Asn Leu
        415                 420                 425
CTG CTT GTG GGT TTT GGC ATC ACC TGT CTC ATC AAC AAC TTA CAC CTC      1465
Leu Leu Val Gly Phe Gly Ile Thr Cys Leu Ile Asn Asn Leu His Leu
    430                 435                 440
CAG TTT GTG ACC TTT GTC CTG CAC ACC ATT GTT CGA GGT TTC TTC CAC      1513
Gln Phe Val Thr Phe Val Leu His Thr Ile Val Arg Gly Phe Phe His
445                 450                 455                 460
TCA GCC TGT GGG AGT CTC TAT GCT GCA GTG TTC CCA TCC AAC CAC TTT      1561
Ser Ala Cys Gly Ser Leu Tyr Ala Ala Val Phe Pro Ser Asn His Phe
                465                 470                 475
GGG ACG CTG ACA GGC CTG CAG TCC CTC ATC AGT GCT GTG TTC GCC TTG      1609
Gly Thr Leu Thr Gly Leu Gln Ser Leu Ile Ser Ala Val Phe Ala Leu
            480                 485                 490
CTT CAG CAG CCA CTT TTC ATG GCG ATG GTG GGA CCC CTG AAA GGA GAG      1657
Leu Gln Gln Pro Leu Phe Met Ala Met Val Gly Pro Leu Lys Gly Glu
        495                 500                 505
CCC TTC TGG GTG AAT CTG GGC CTC CTG CTA TTC TCA CTC CTG GGA TTC      1705
Pro Phe Trp Val Asn Leu Gly Leu Leu Leu Phe Ser Leu Leu Gly Phe
    510                 515                 520
CTG TTG CCT TCC TAC CTC TTC TAT TAC CGT GCC CGG CTC CAG CAG GAG      1753
Leu Leu Pro Ser Tyr Leu Phe Tyr Tyr Arg Ala Arg Leu Gln Gln Glu
525                 530                 535                 540
TAC GCC GCC AAT GGG ATG GGC CCA CTG AAG GTG CTT AGC GGC TCT GAG      1801
Tyr Ala Ala Asn Gly Met Gly Pro Leu Lys Val Leu Ser Gly Ser Glu
                545                 550                 555
GTG ACC GCA TAGACTTCTC AGACCAAGGG ACCTGGATGA                          1840
Val Thr Ala

CAGGCAATCA AGGCCTGAGC AACCAAAAGG AGTGCCCCAT ATGGCTTTTC TACCTGTAAC    1900
ATGCACATAG AGCCATGGCC GTAGATTTAT AAATACCAAG AGAAGTTCTA TTTTTGTAAA    1960
GACTGCAAAA AGGAGGAAAA AAAAACCTTC AAAAACGCCC CCTAAGTCAA CGCTCCATTG    2020
ACTGAAGACA GTCCCTATCC TAGAGGGGTT GAGCCTTCTT CCTCCTTGGG TTGGAGGAGA    2080
CCAGGGTGCC TCTTATCTCC TTCTAGCGGT CTGCCTCCTG GTACCTCTTG GGGGGATCGG    2140
CAAACAGGCT ACCCCTGAGG TCCCATGTGC CATGAGTGTG CACACATGCA TGTGTCTGTG    2200
TATGTGTGAA TGTGAGAGAG ACACAGCCCT CCTTTCAGAA GGAAAGGGGC CTGAGGTGCC    2260
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AGCTGTGTCC TGGGTTAGGG GTTGGGGGTC GGCCCCTTCC AGGGCCAGGA GGGCAGGTTC 2320
CCTCTCTGGT GCTGCTGCTT GCAAGTCTTA GAGGAAATAA AAAGGGAAGT GAG 2373

Sequence No.: 72
Sequence length: 1316
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Osterosarcoma
  Cell line: U-2 OS
  Clone name: HP10304
Sequence characteristics
  Code representing characteristics: CDS
  Existence site: 11.. 1003
  Characterization method: E
Sequence description

```
GTTGTCCAAG ATG GAG GGC GCT CCA CCG GGG TCG CTC GCC CTC CGG CTC      49
           Met Glu Gly Ala Pro Pro Gly Ser Leu Ala Leu Arg Leu
             1               5                  10
CTG CTG TTC GTG GCG CTA CCC GCC TCC GGC TGG CTG ACG ACG GGC GCC      97
Leu Leu Phe Val Ala Leu Pro Ala Ser Gly Trp Leu Thr Thr Gly Ala
     15                  20                  25
CCC GAG CCG CCG CCG CTG TCC GGA GCC CCA CAG GAC GGC ATC AGA ATT     145
Pro Glu Pro Pro Pro Leu Ser Gly Ala Pro Gln Asp Gly Ile Arg Ile
 30                  35                  40                  45
AAT GTA ACT ACA CTG AAA GAT GAT GGG GAC ATA TCT AAA CAG CAG GTT     193
Asn Val Thr Thr Leu Lys Asp Asp Gly Asp Ile Ser Lys Gln Gln Val
                 50                  55                  60
GTT CTT AAC ATA ACC TAT GAG AGT GGA CAG GTG TAT GTA AAT GAC TTA     241
Val Leu Asn Ile Thr Tyr Glu Ser Gly Gln Val Tyr Val Asn Asp Leu
             65                  70                  75
CCT GTA AAT AGT GGT GTA ACC CGA ATA AGC TGT CAG ACT TTG ATA GTG     289
Pro Val Asn Ser Gly Val Thr Arg Ile Ser Cys Gln Thr Leu Ile Val
         80                  85                  90
AAG AAT GAA AAT CTT GAA AAT TTG GAG GAA AAA GAA TAT TTT GGA ATT     337
Lys Asn Glu Asn Leu Glu Asn Leu Glu Glu Lys Glu Tyr Phe Gly Ile
     95                 100                 105
GTC AGT GTA AGG ATT TTA GTT CAT GAG TGG CCT ATG ACA TCT GGT TCC     385
Val Ser Val Arg Ile Leu Val His Glu Trp Pro Met Thr Ser Gly Ser
```

110 115 120 125
AGT TTG CAA CTA ATT GTC ATT CAA GAA GAG GTA GTA GAG ATT GAT GGA 433
Ser Leu Gln Leu Ile Val Ile Gln Glu Glu Val Val Glu Ile Asp Gly
130 135 140
AAA CAA GTT CAG CAA AAG GAT GTC ACT GAA ATT GAT ATT TTA GTT AAG 481
Lys Gln Val Gln Gln Lys Asp Val Thr Glu Ile Asp Ile Leu Val Lys
145 150 155
AAC CGG GGA GTA CTC AGA CAT TCA AAC TAT ACC CTC CCT TTG GAA GAA 529
Asn Arg Gly Val Leu Arg His Ser Asn Tyr Thr Leu Pro Leu Glu Glu
160 165 170
AGC ATG CTC TAC TCT ATT TCT CGA GAC AGT GAC ATT TTA TTT ACC CTT 577
Ser Met Leu Tyr Ser Ile Ser Arg Asp Ser Asp Ile Leu Phe Thr Leu
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CCT AAC CTC TCC AAA AAA GAA AGT GTT AGT TCA CTG CAA ACC ACT AGC 625
Pro Asn Leu Ser Lys Lys Glu Ser Val Ser Ser Leu Gln Thr Thr Ser
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CAG TAT CTT ATC AGG AAT GTG GAA ACC ACT GTA GAT GAA GAT GTT TTA 673
Gln Tyr Leu Ile Arg Asn Val Glu Thr Thr Val Asp Glu Asp Val Leu
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CCT GGC AAG TTA CCT GAA ACT CCT CTC AGA GCA GAG CCG CCA TCT TCA 721
Pro Gly Lys Leu Pro Glu Thr Pro Leu Arg Ala Glu Pro Pro Ser Ser
225 230 235
TAT AAG GTA ATG TGT CAG TGG ATG GAA AAG TTT AGA AAA GAT CTG TGT 769
Tyr Lys Val Met Cys Gln Trp Met Glu Lys Phe Arg Lys Asp Leu Cys
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Arg Phe Trp Ser Asn Val Phe Pro Val Phe Phe Gln Phe Leu Asn Ile
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ATG GTG GTT GGA ATT ACA GGA GCA GCT GTG GTA ATA ACC ATC TTA AAG 865
Met Val Val Gly Ile Thr Gly Ala Ala Val Val Ile Thr Ile Leu Lys
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GTG TTT TTC CCA GTT TCT GAA TAC AAA GGA ATT CTT CAG TTG GAT AAA 913
Val Phe Phe Pro Val Ser Glu Tyr Lys Gly Ile Leu Gln Leu Asp Lys
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Val Asp Val Ile Pro Val Thr Ala Ile Asn Leu Tyr Pro Asp Gly Pro
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Sequence length: 893
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Strandedness: Double
Topology: Linear
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  Cell kind: Osterosarcoma
  Cell line: U-2 OS
  Clone name: HP10305
Sequence characteristics
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  Existence site: 110.. 436
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Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe Pro Phe Cys
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Asp Gly Ala His Thr Lys His Asn Glu Glu Thr Gly Asp Asn Val Gly
    85                  90                  95
CCT CTG ATC ATC AAG AAA AAA GAA ACT TAAATGGACA CTTTTGA             450
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Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
  Organism species: *Homo sapiens*
  Cell kind: Osterosarcoma
  Cell line: U-2 OS
  Clone name: HP10306
Sequence characteristics
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  Existence site: 230.. 535
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Met Asn Leu
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Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe Leu Phe Trp
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Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile Tyr Arg Pro
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CGC TGG GGT GCC CTT GGG GAC TAC CTC TCC TTC ACC ATA CCC CTG GGC 526
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ACC CCC TGACAACTTC TGCACATACT GGGGCCCTGC TTATTCTCCC AGGACAGG 580
Thr Pro
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Sequence No.: 75
Sequence length: 2186
Sequence type: Nucleic acid
Strandedness: Double
Topology: Linear
Sequence kind: cDNA to mRNA
Original source:
Organism species: *Homo sapiens*
Cell kind: Epidermoid carcinoma
Cell line: KB
Clone name: HP10328
Sequence characteristics
Code representing characteristics: CDS
Existence site: 118.. 1236
Characterization method: E
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Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala
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AATATAAAAT TTTGTG 2186

Claims

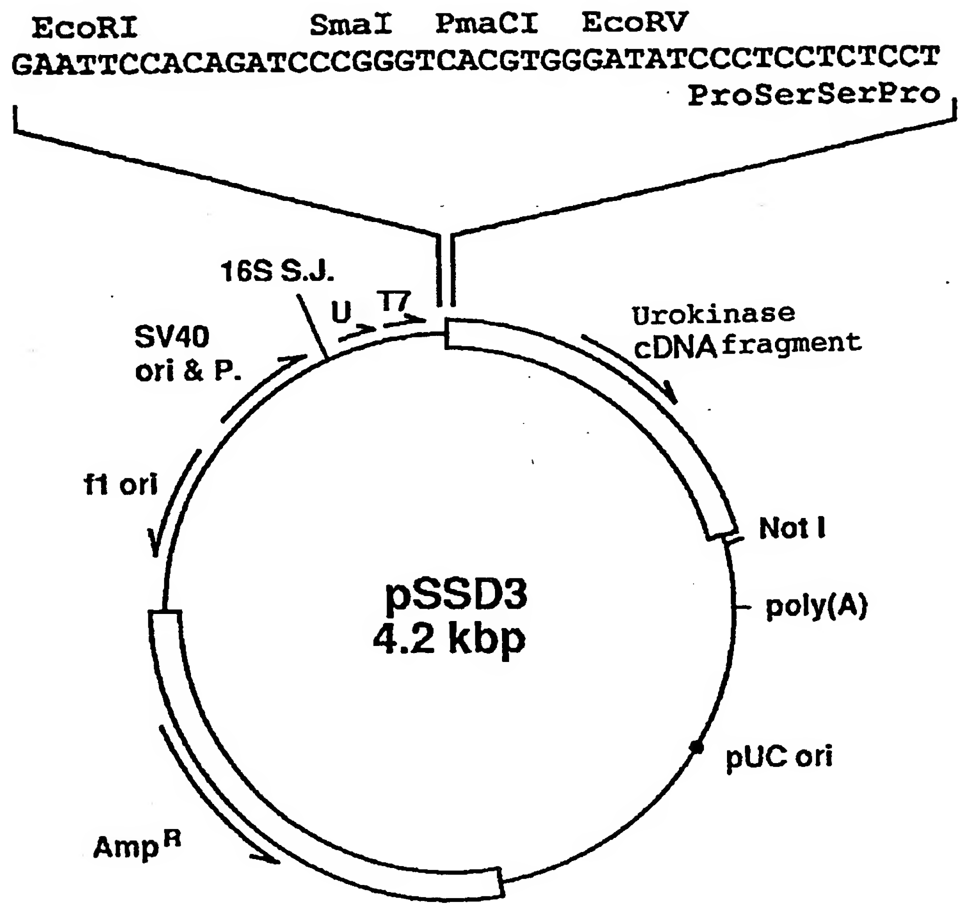
1. A protein containing any of the amino acid sequences represented by Sequence No. 1 to Sequence No. 2 or by Sequence No. 4 to Sequence No. 25.

2. A DNA encoding any of the proteins as described in Claim 1.

3. A cDNA containing any of the base sequences represented by Sequence No. 26 to Sequence No. 50.

4. A cDNA as described in Claim 3 which comprises any of the base sequences represented by Sequence No. 51 to Sequence No. 75.

5. A transformed eukaryotic cell capable of expressing any of DNAs as described in Claim 2 to 4 and producing a protein as described in Claim 1.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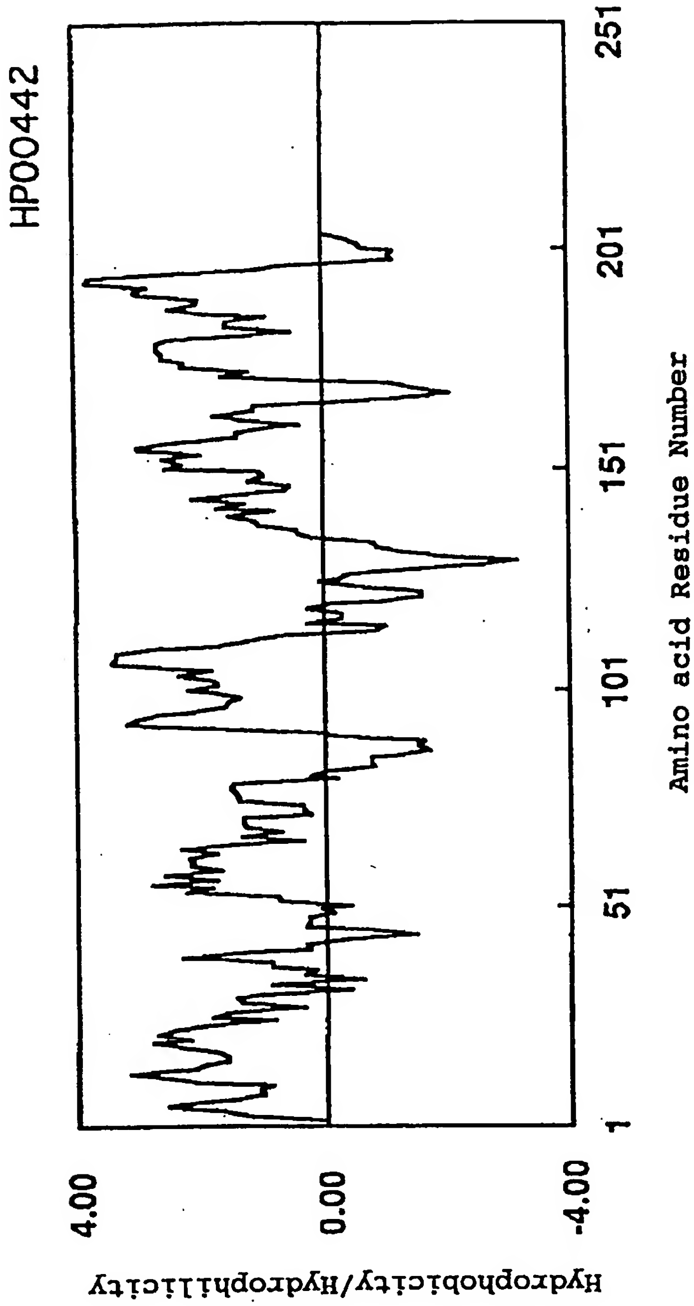
16S S.J.
U
T7
SV40
ori & P.
Urokinase
cDNA fragment
f1 ori
Not I
pSSD3
4.2 kbp
poly(A)
pUC ori
Amp R

Fig. 1

Fig. 2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Hydrophobicity/Hydrophilicity
Amino acid Residue Number

Fig. 3

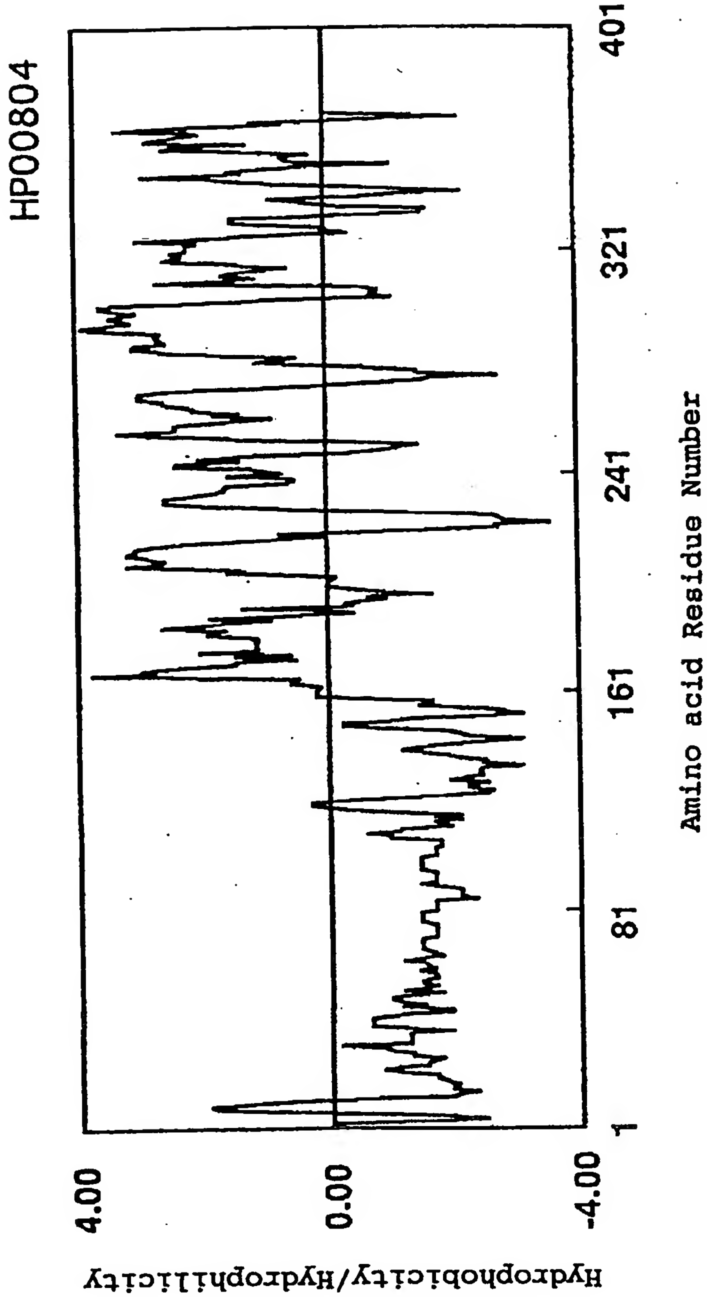
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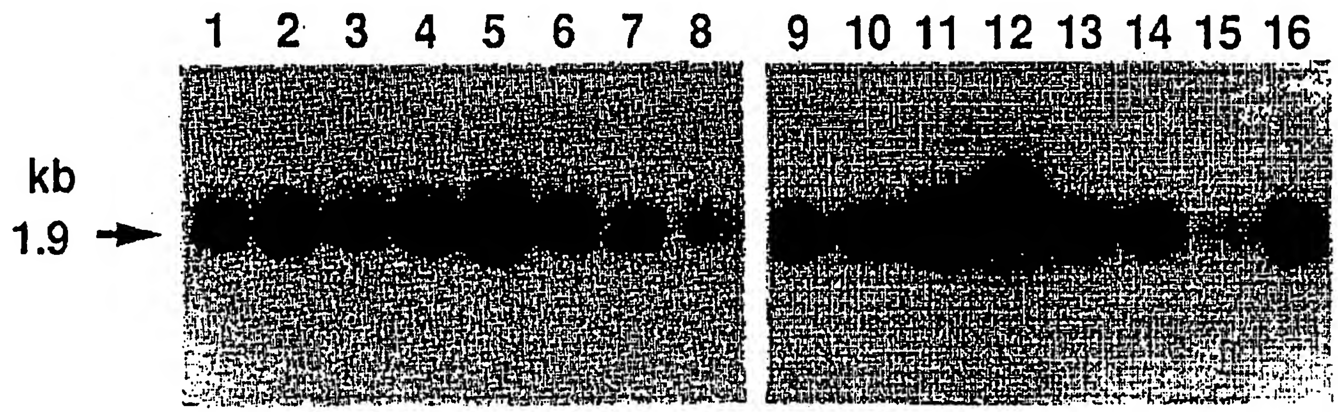
Fig. 4



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2 Brain
3 Placenta
4 Lung
5 Liver
6 Skeletal muscle
7 Kidney
8 Pancreas

9 spleen
10 Thymus
11 Prostate
12 Testis
13 Ovary
14 Small intestine
15 Large intestine
16 Peripheral blood leukocyte

Fig. 5

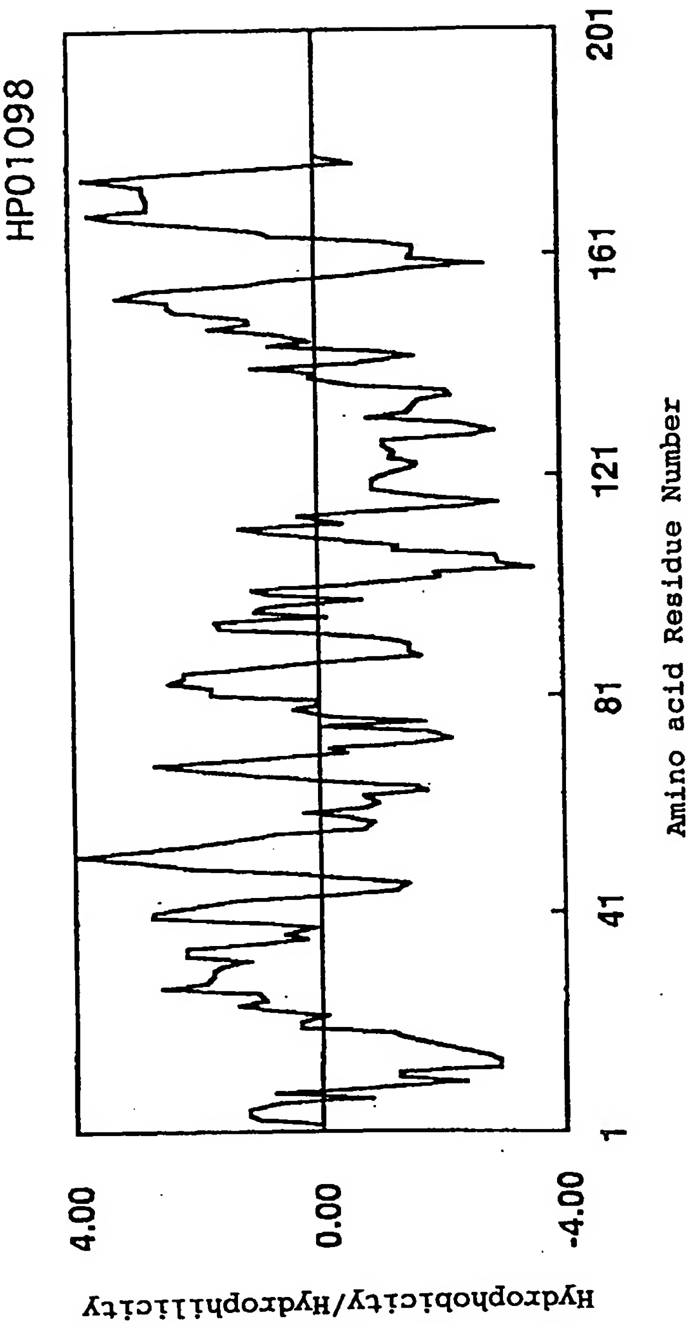
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Fig. 6

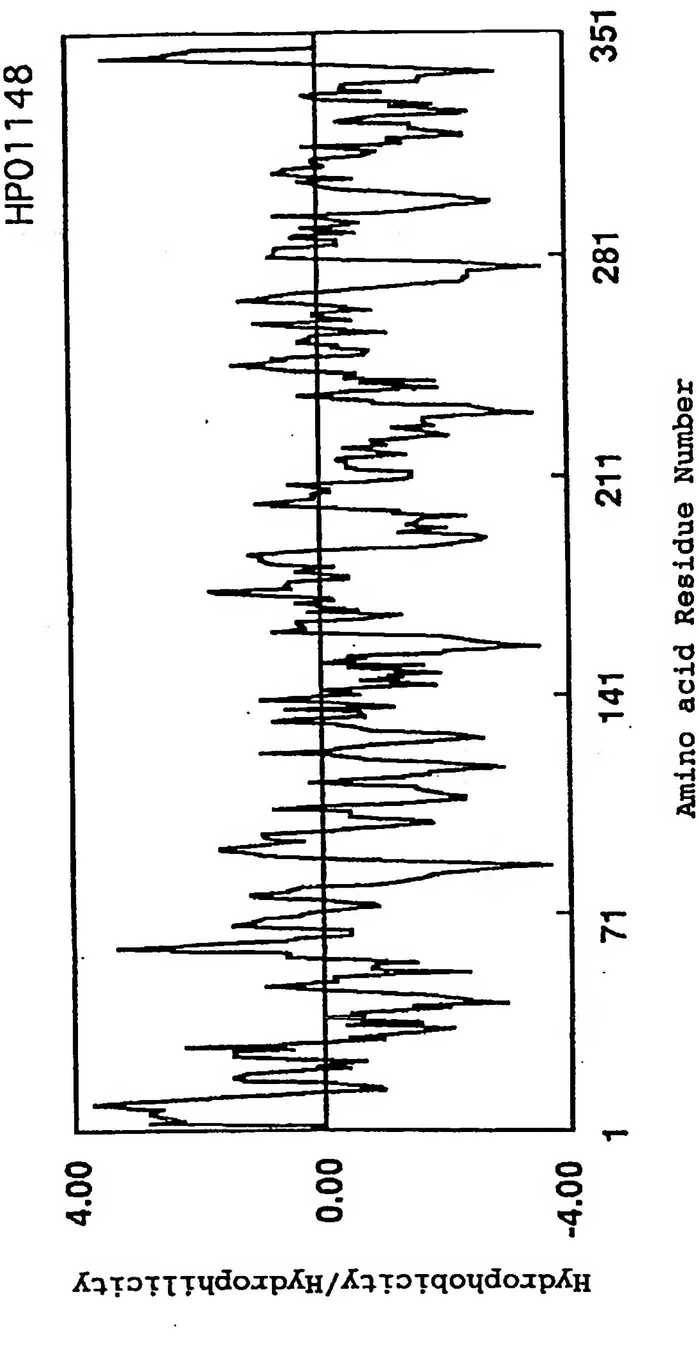
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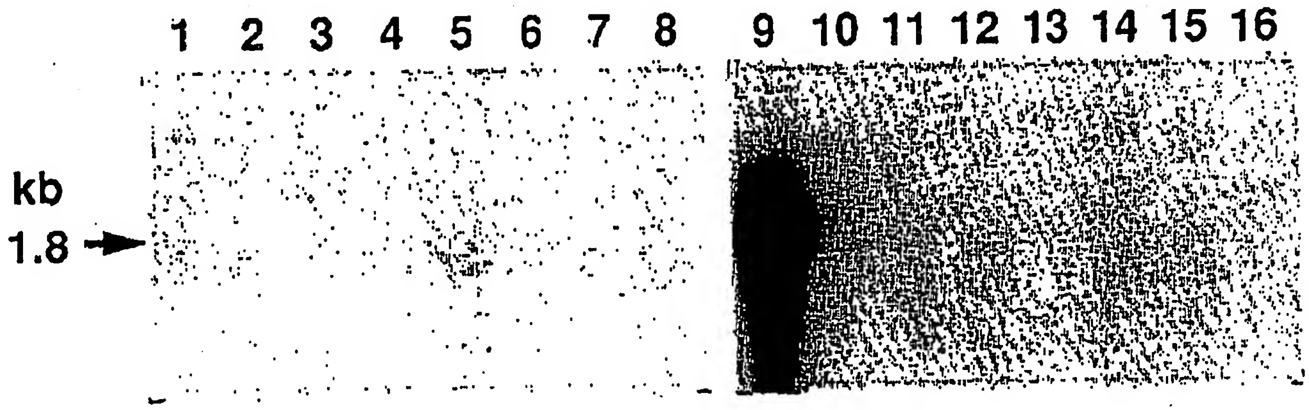
Fig. 7



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2 Brain
3 Placenta
4 Lung
5 Liver
6 Skeletal muscle
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14 Small intestine
15 Large intestine
16 Peripheral blood leukocyte

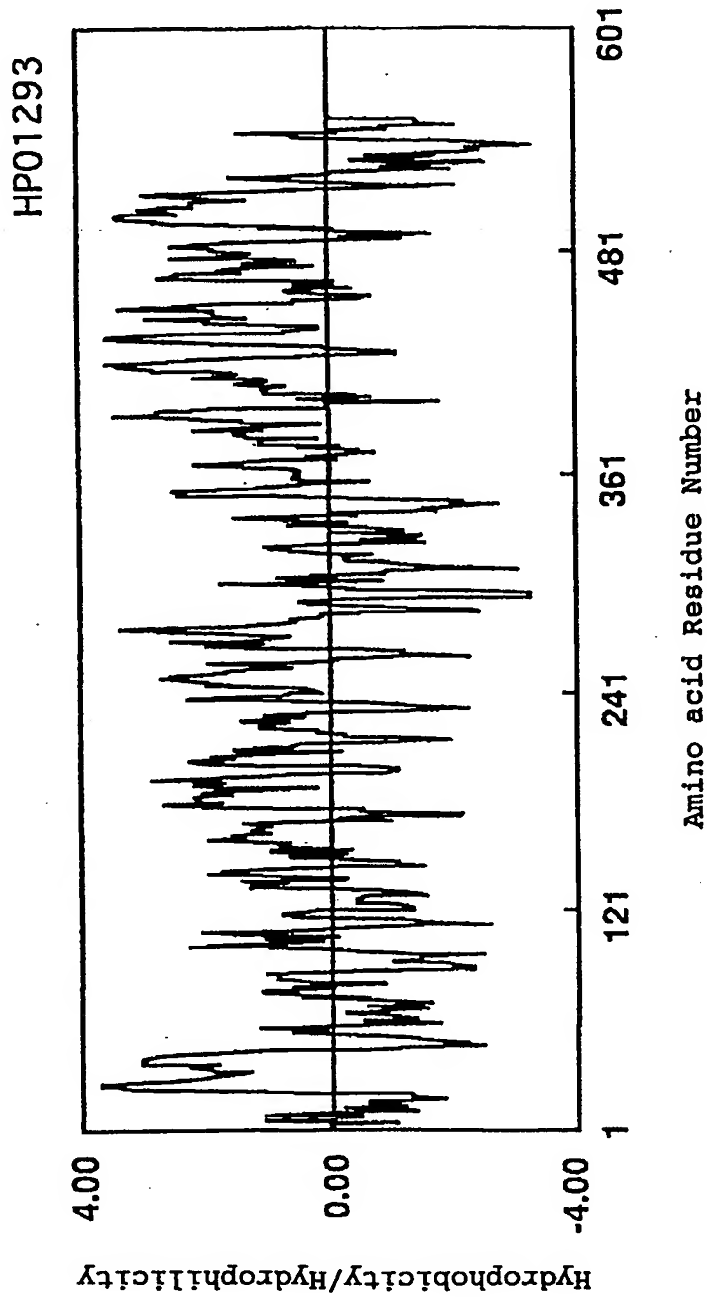
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Fig. 8

Fig. 9

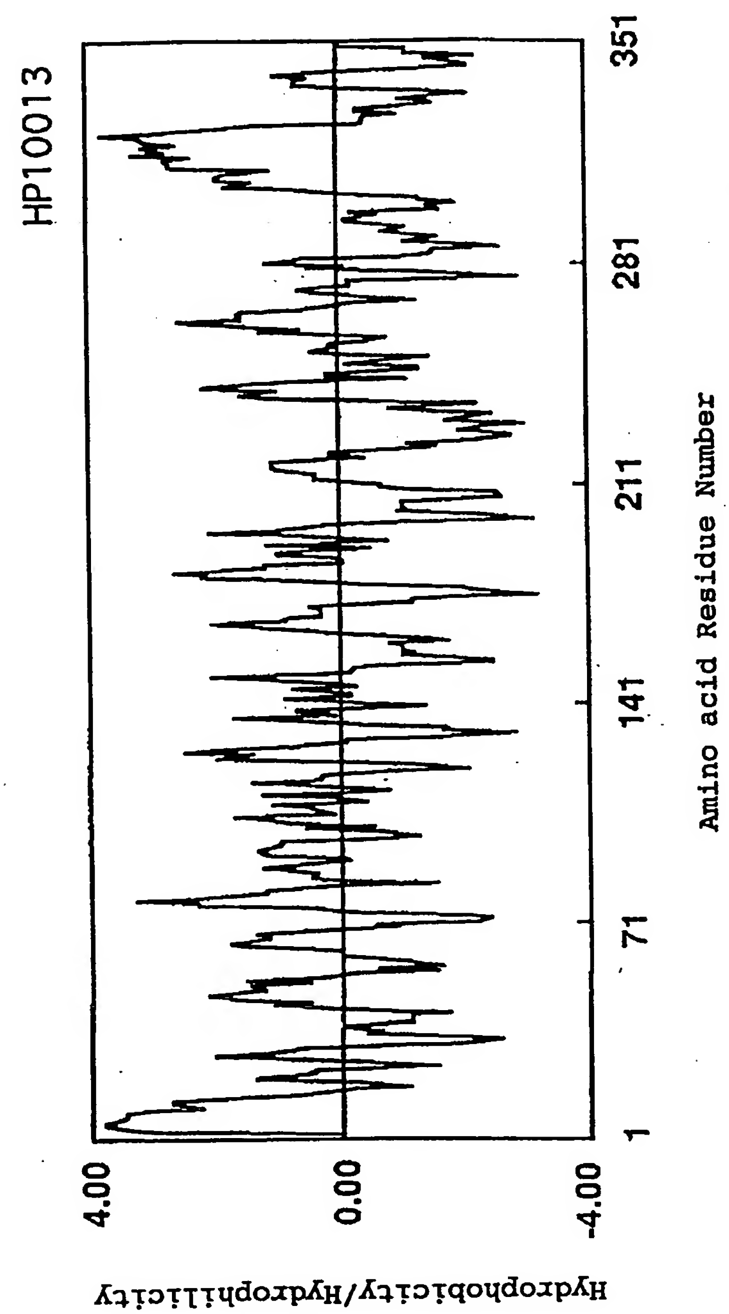
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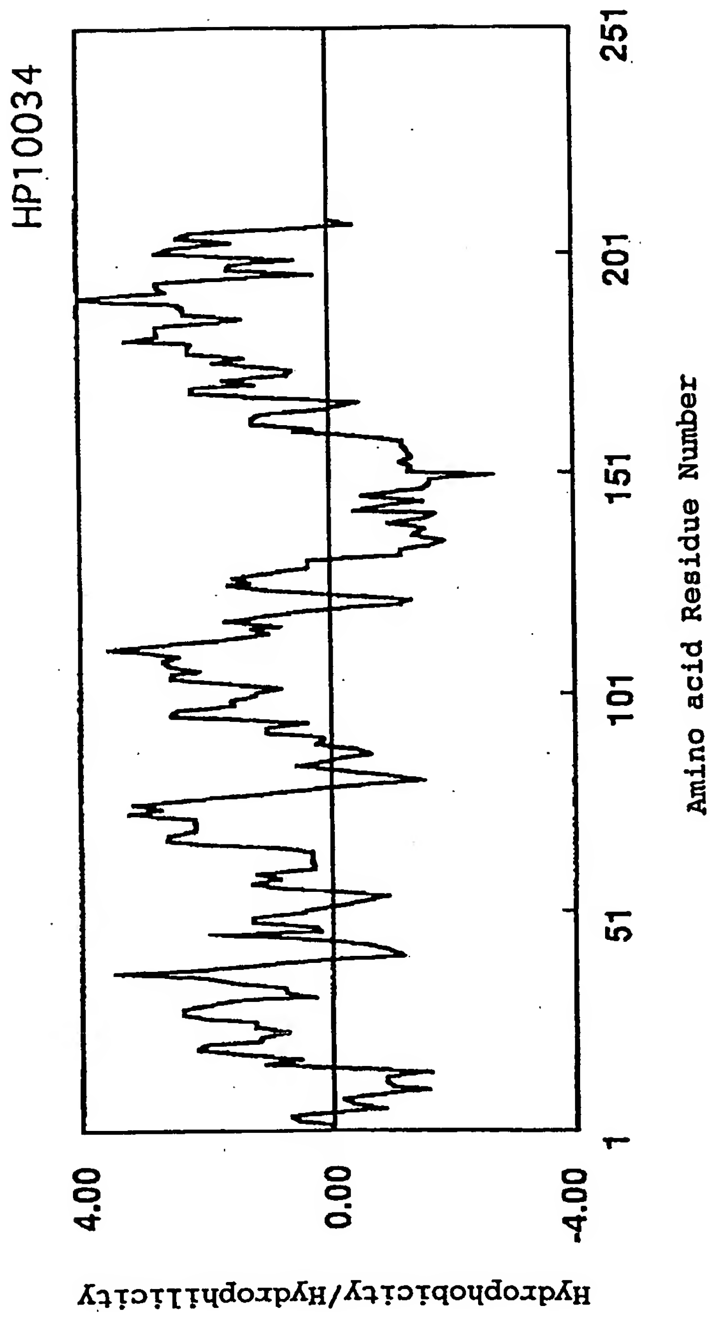
Fig. 10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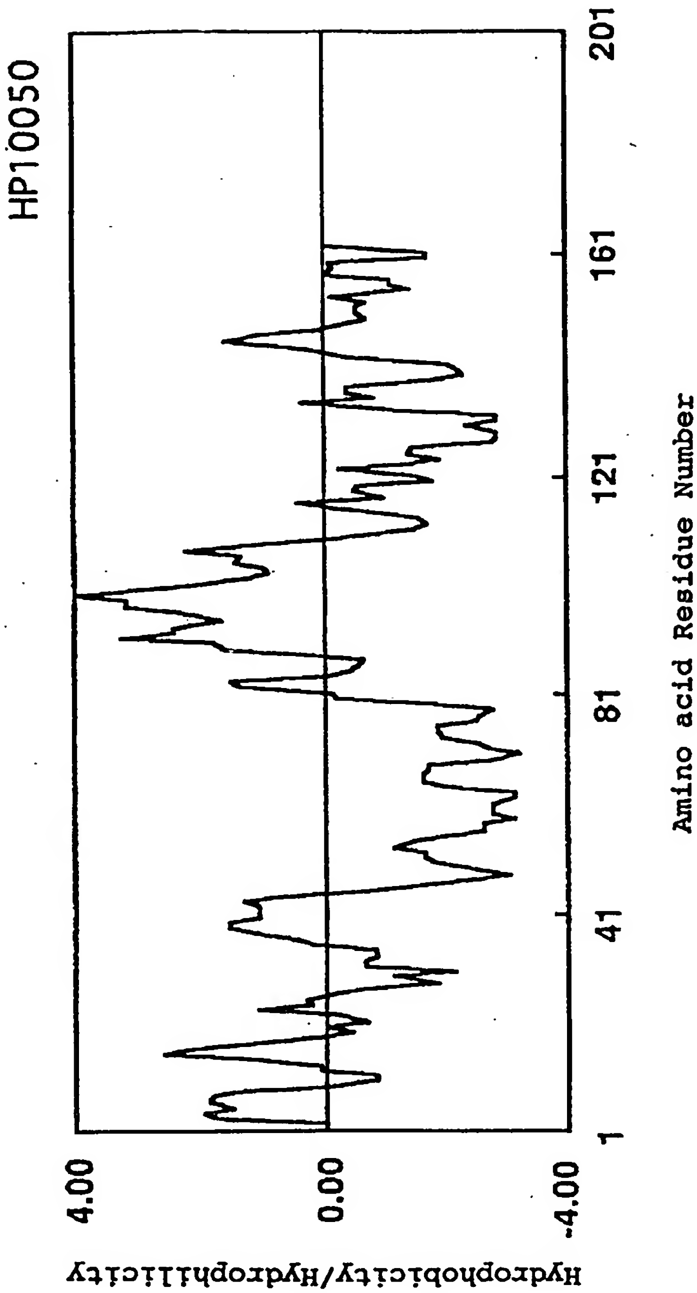
Amino acid Residue Number

Fig. 11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Hydrophobicity/Hydrophilicity

Fig. 12

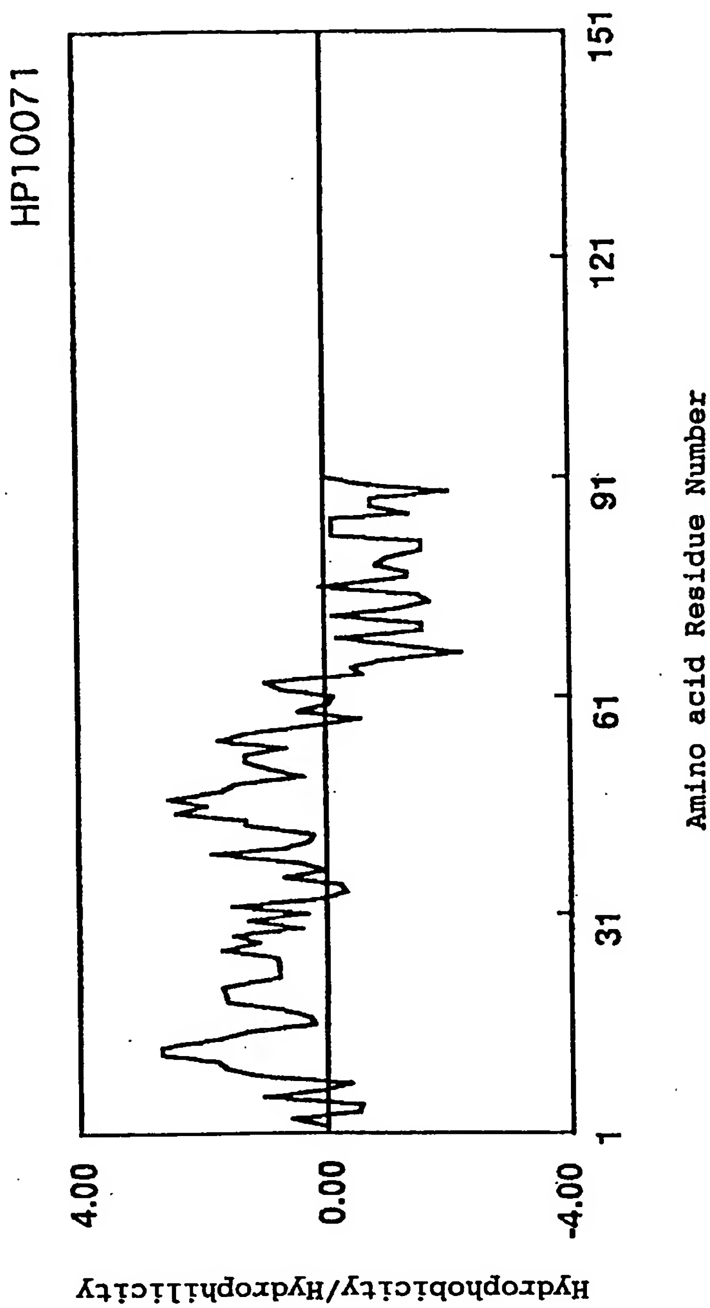
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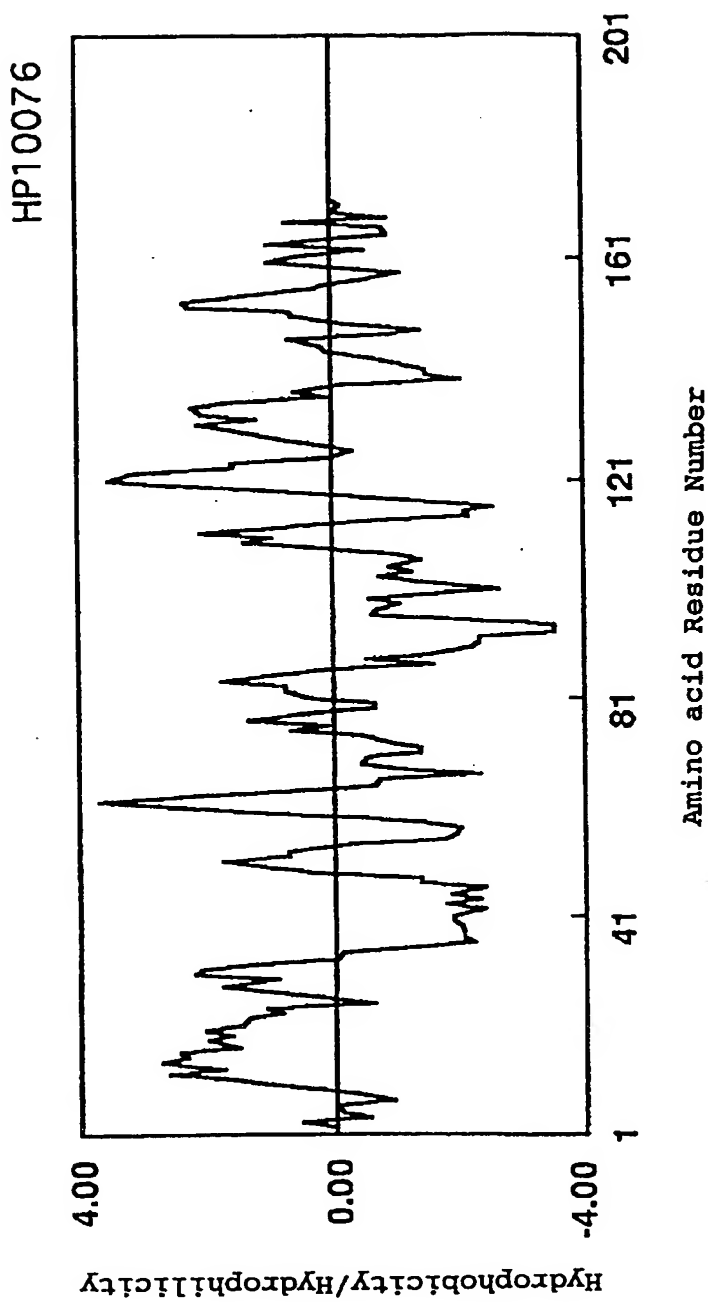
Fig. 13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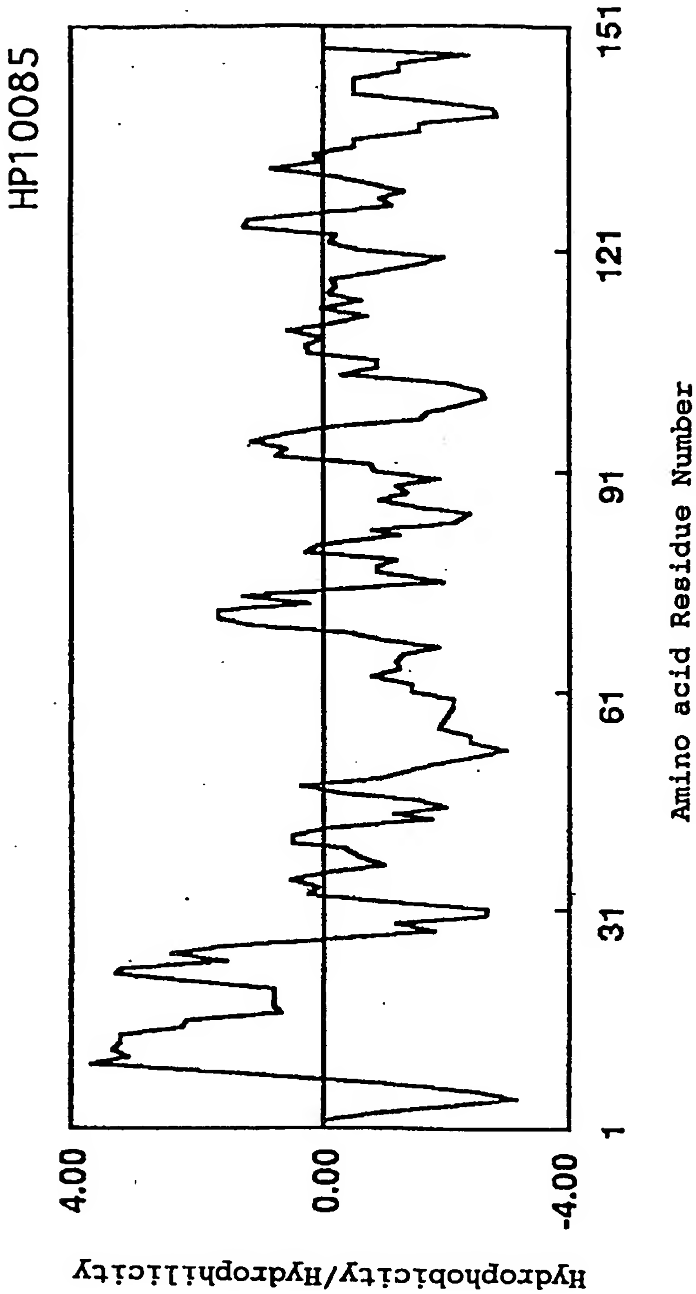
Hydrophobicity/Hydrophilicity

Fig. 14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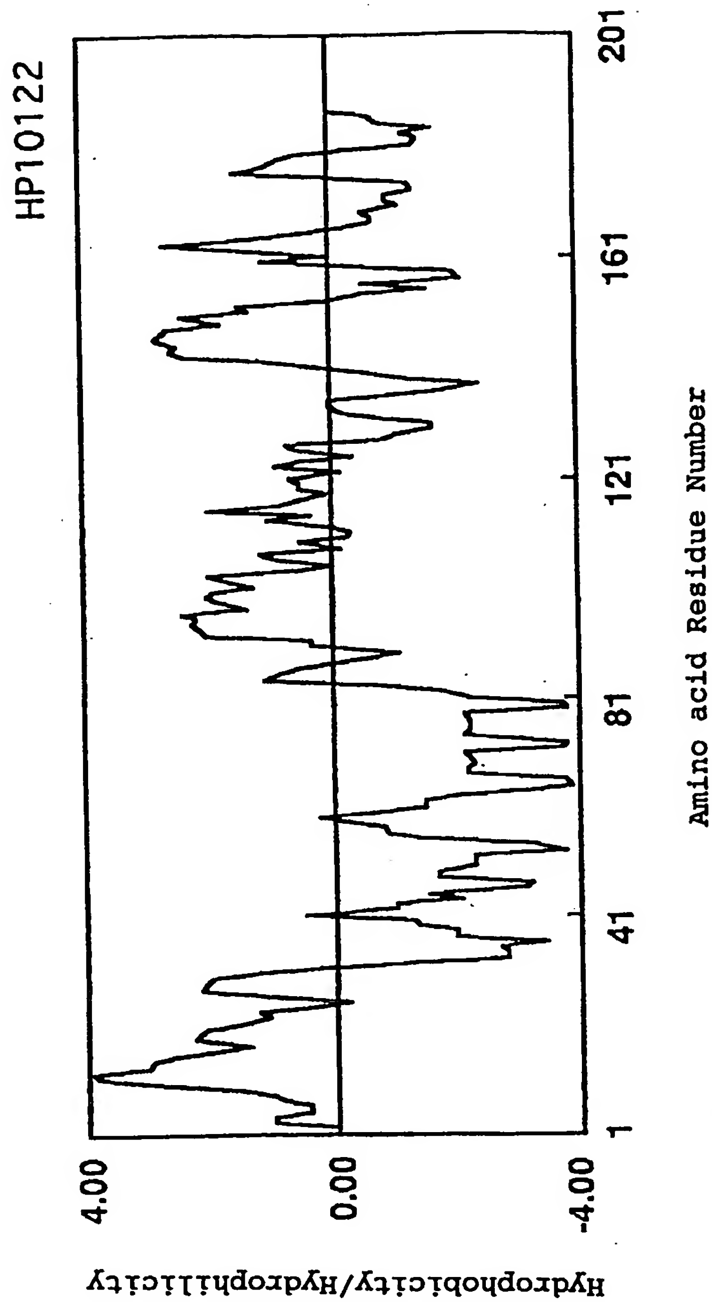
151
Amino acid Residue Number

Fig. 15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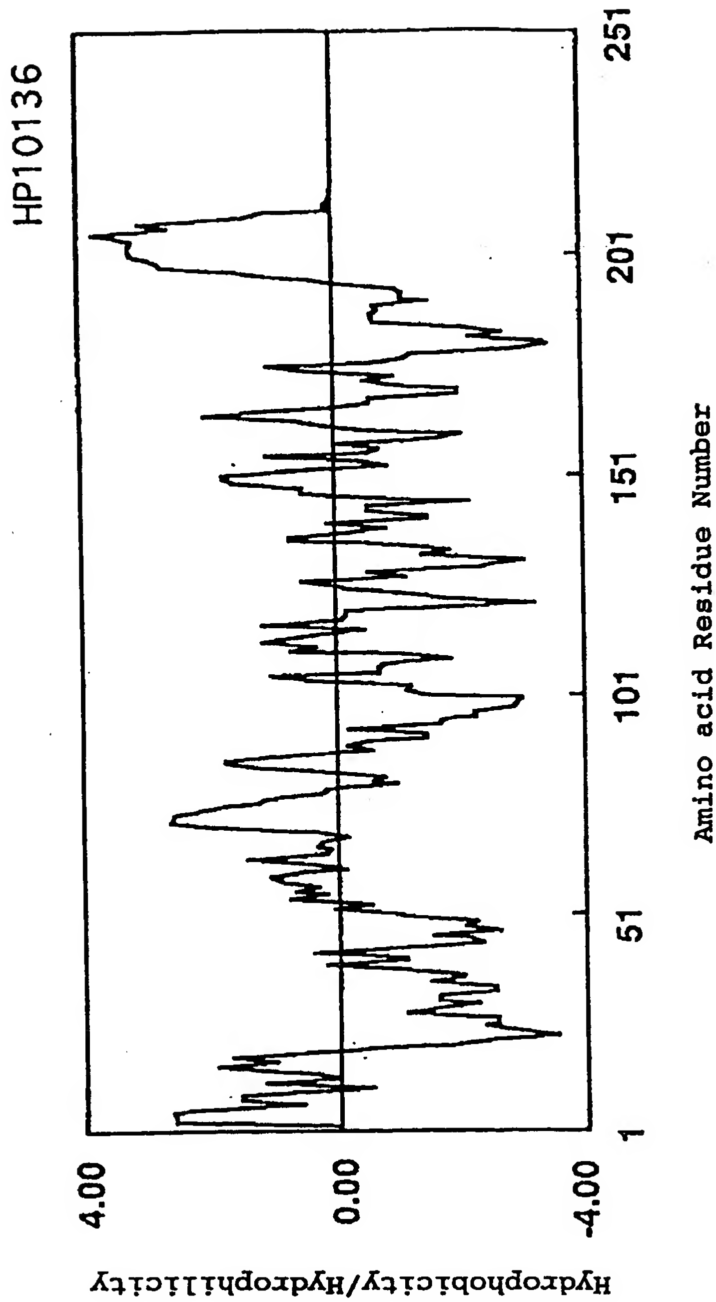
Amino acid Residue Number
Hydrophobicity/Hydrophilicity

Fig. 16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Amino acid Residue Number

Fig. 17

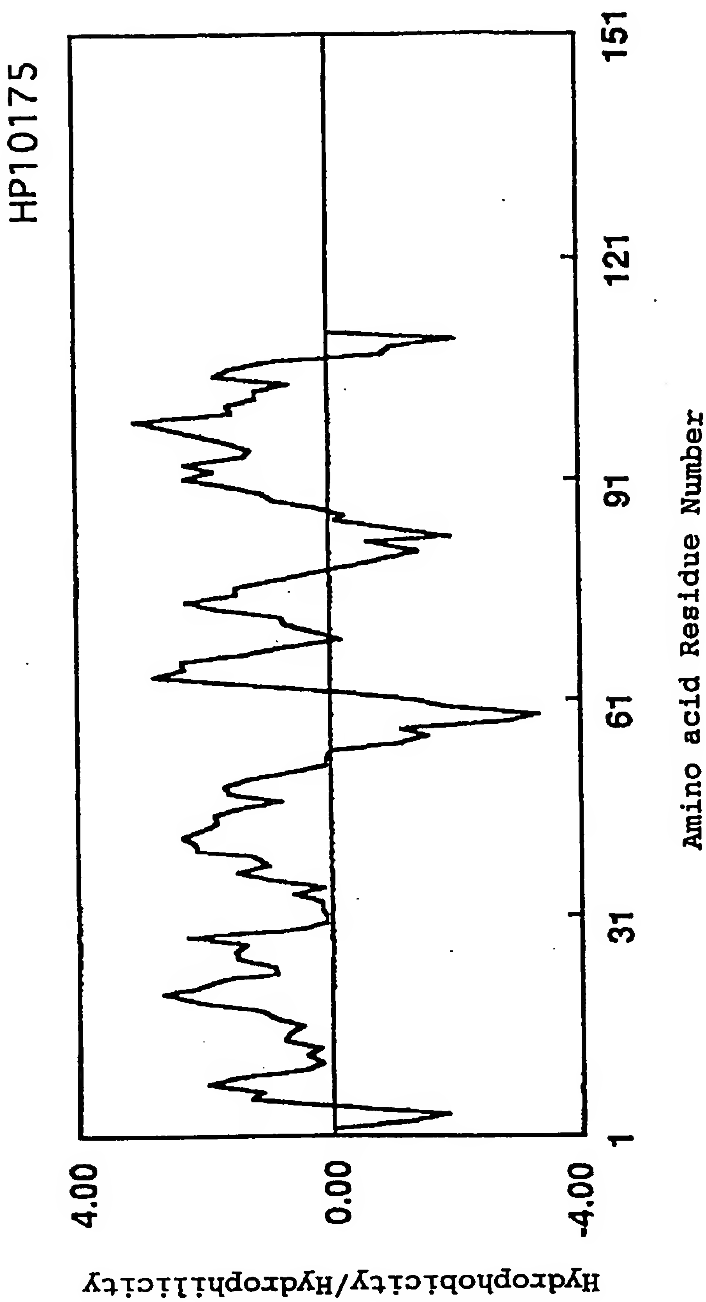
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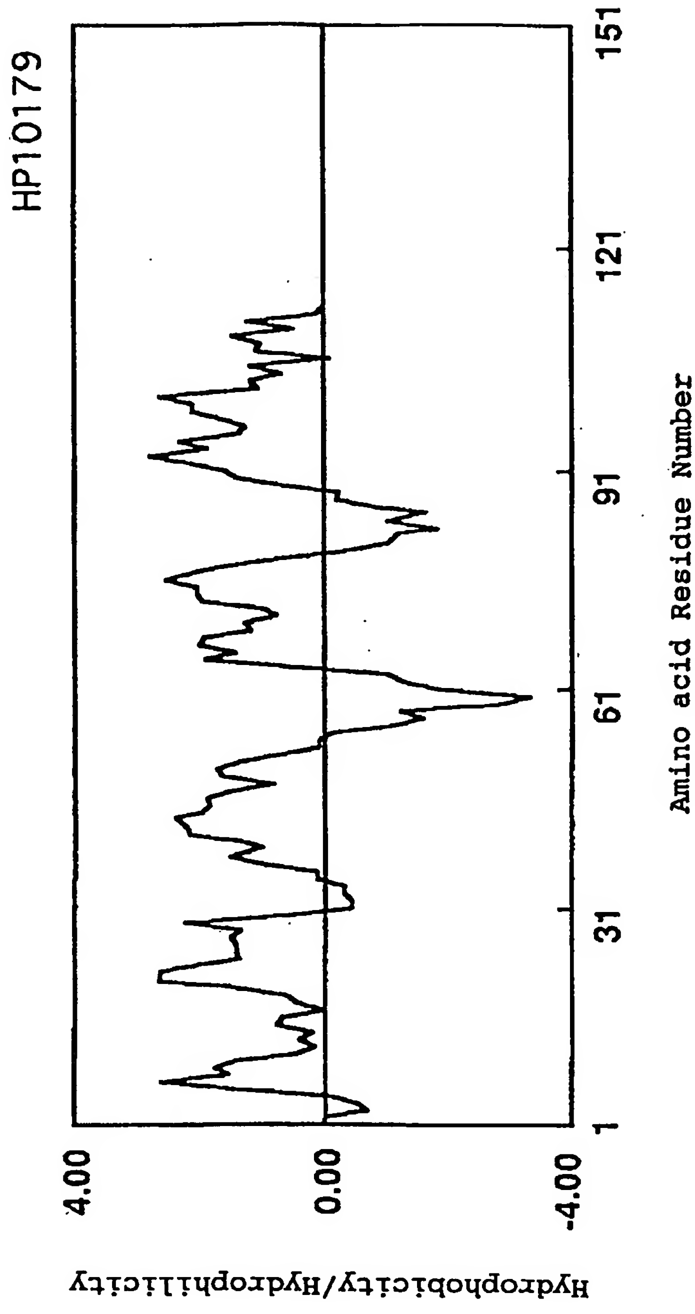
Fig. 18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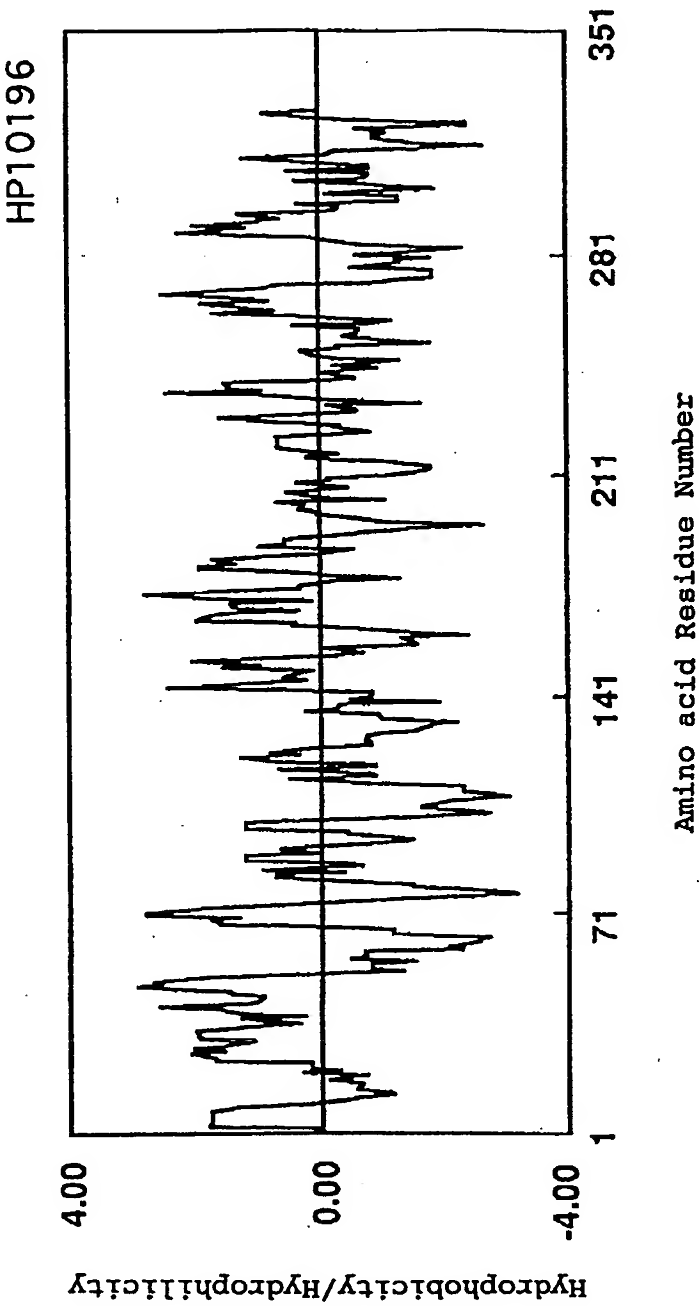
Hydrophobicity/Hydrophilicity

Fig. 19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Hydrophobicity/Hydrophilicity
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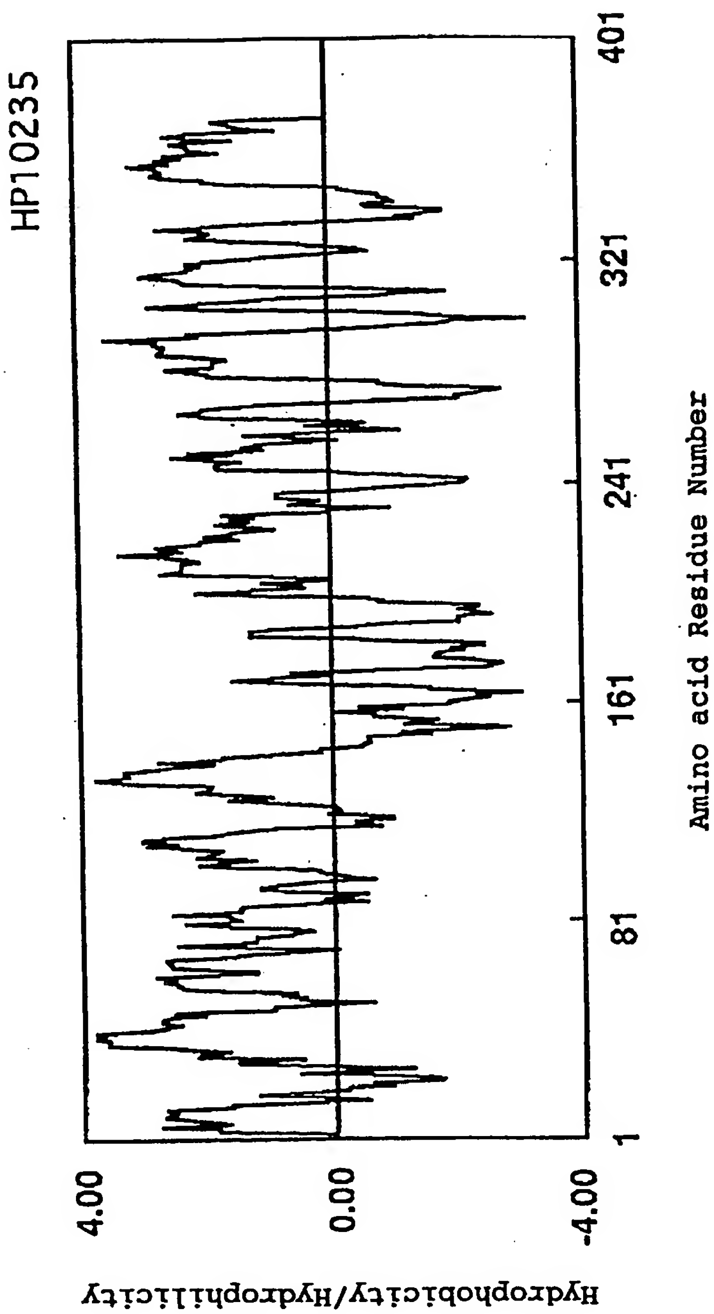
281
351
Amino acid Residue Number

Fig. 20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Amino acid Residue Number
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161
241
321
401

Fig. 21

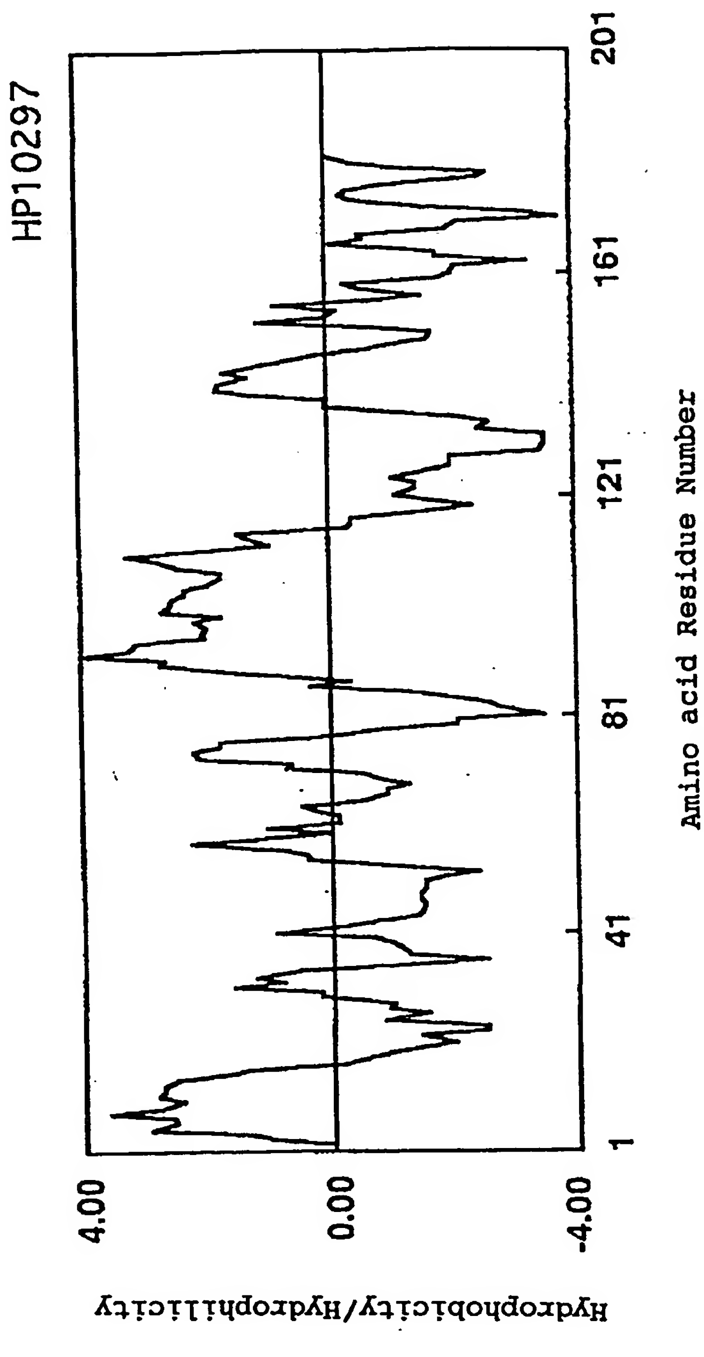

HP10297
4.00
0.00
-4.00
Hydrophobicity/Hydrophilicity
1
41
81
121
161
201
Amino acid Residue Number

Fig. 22

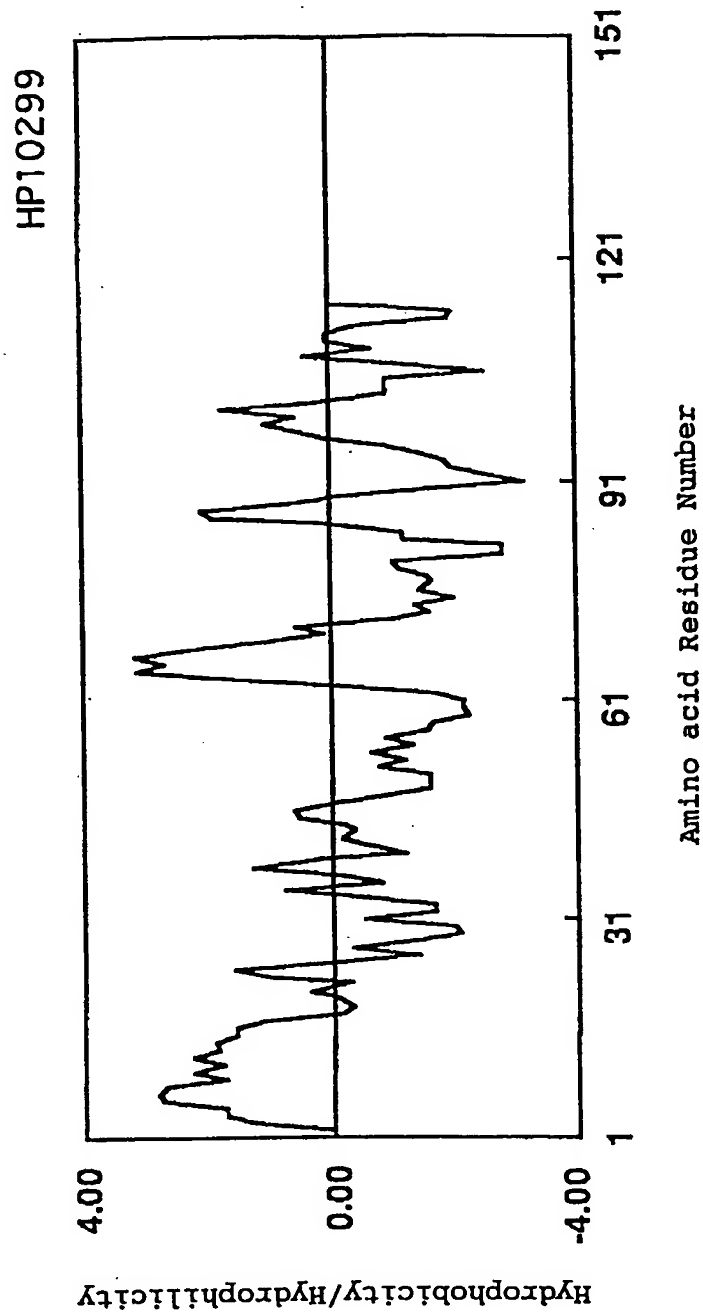

HP10299
4.00
0.00
-4.00
1
31
61
91
121
151
Amino acid Residue Number
Hydrophobicity/Hydrophilicity

Fig. 23

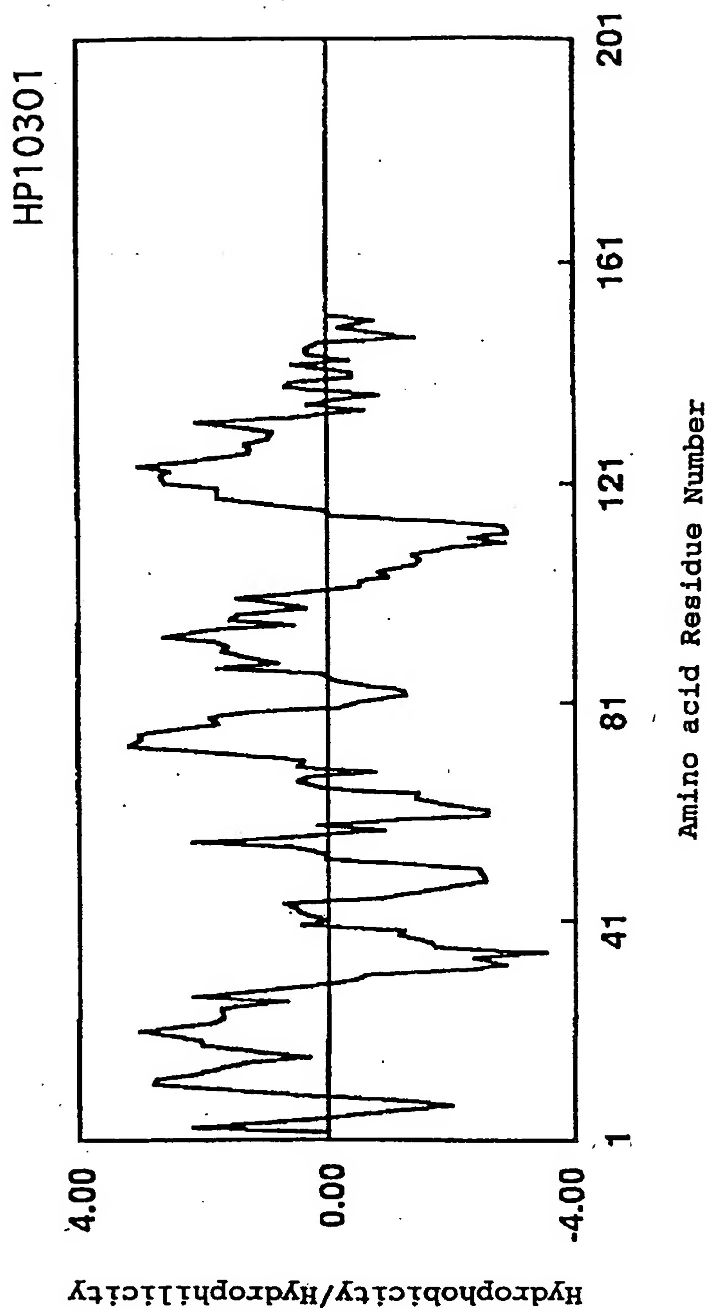

HP10301
4.00
0.00
-4.00
1
41
81
121
161
201
Amino acid Residue Number
Hydrophobicity/Hydrophilicity

Fig. 24

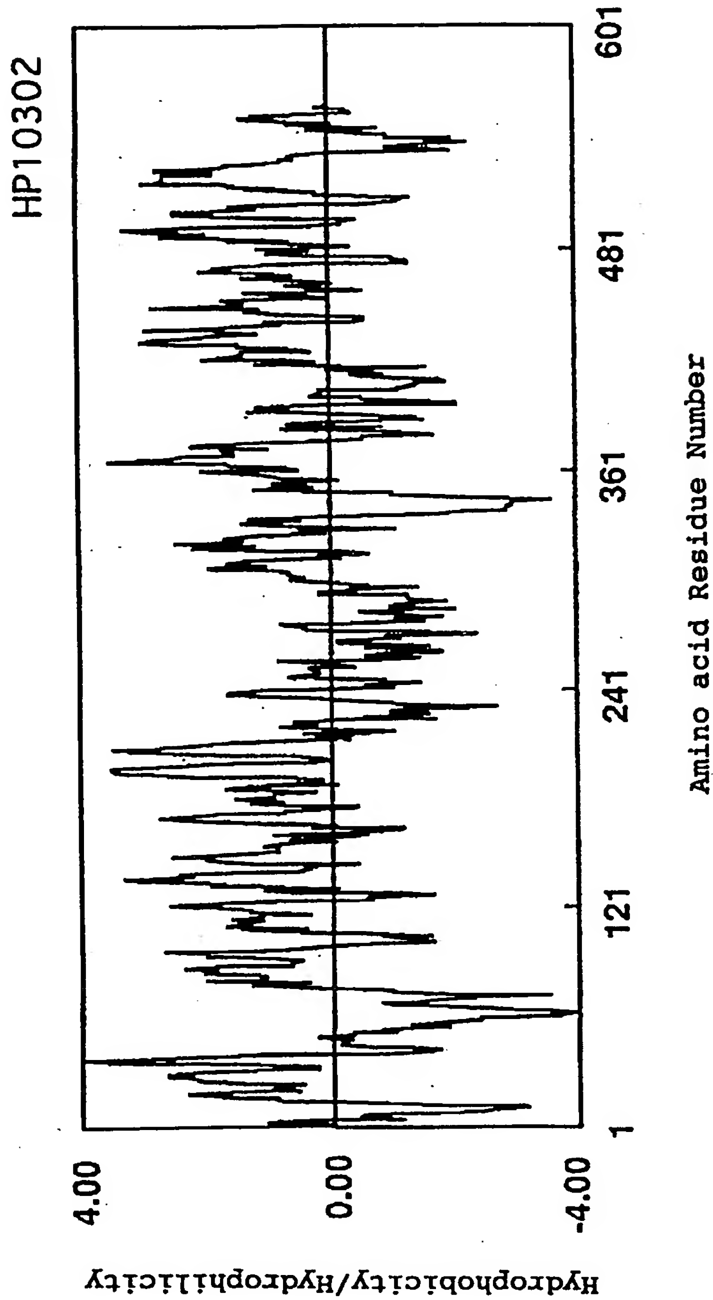

HP10302
Hydrophobicity/Hydrophilicity
4.00
0.00
-4.00
Amino acid Residue Number
1
121
241
361
481
601

Fig. 25

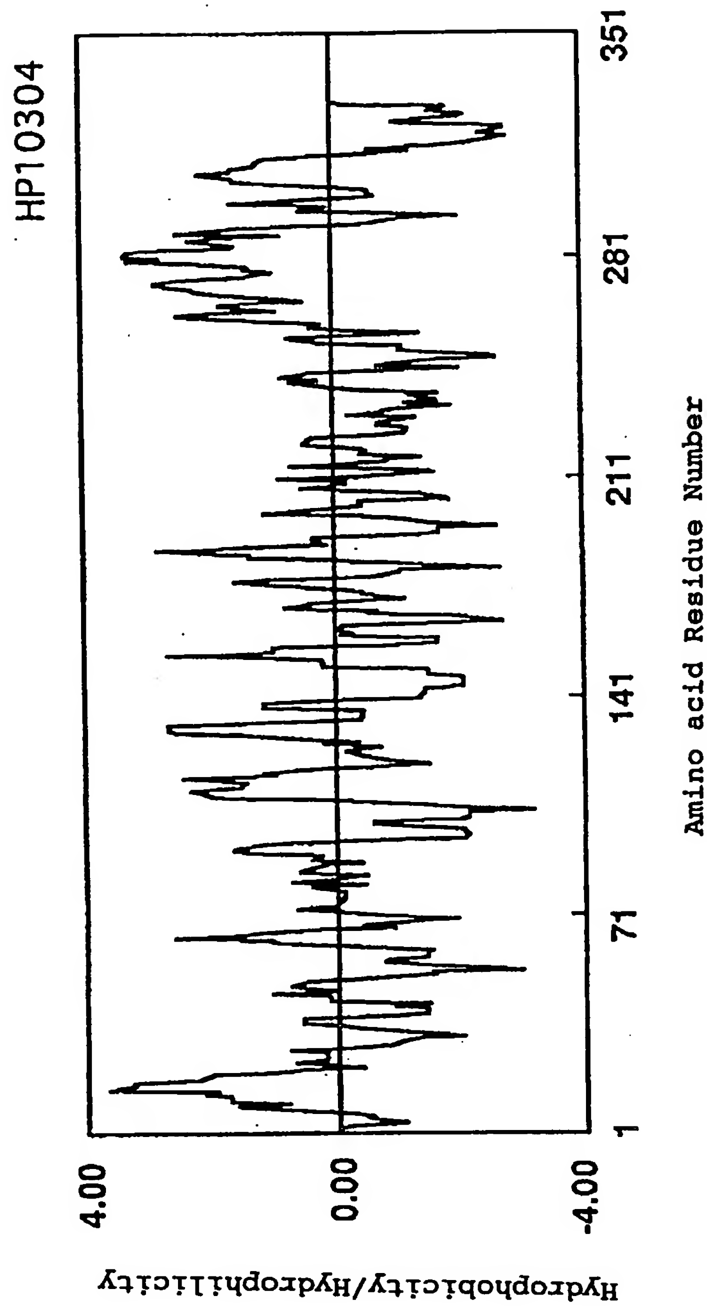

HP10304
4.00
0.00
-4.00
1
71
141
211
281
351
Amino acid Residue Number
Hydrophobicity/Hydrophilicity

Fig. 26

HP10305

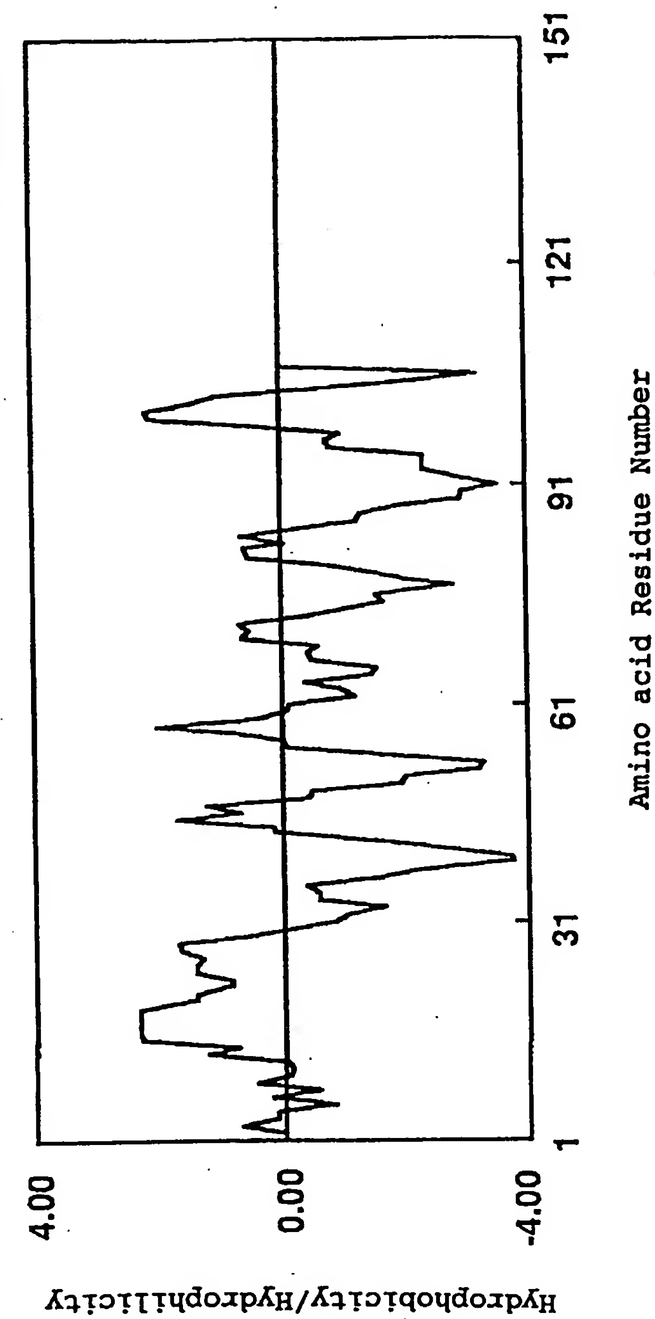


Fig. 27

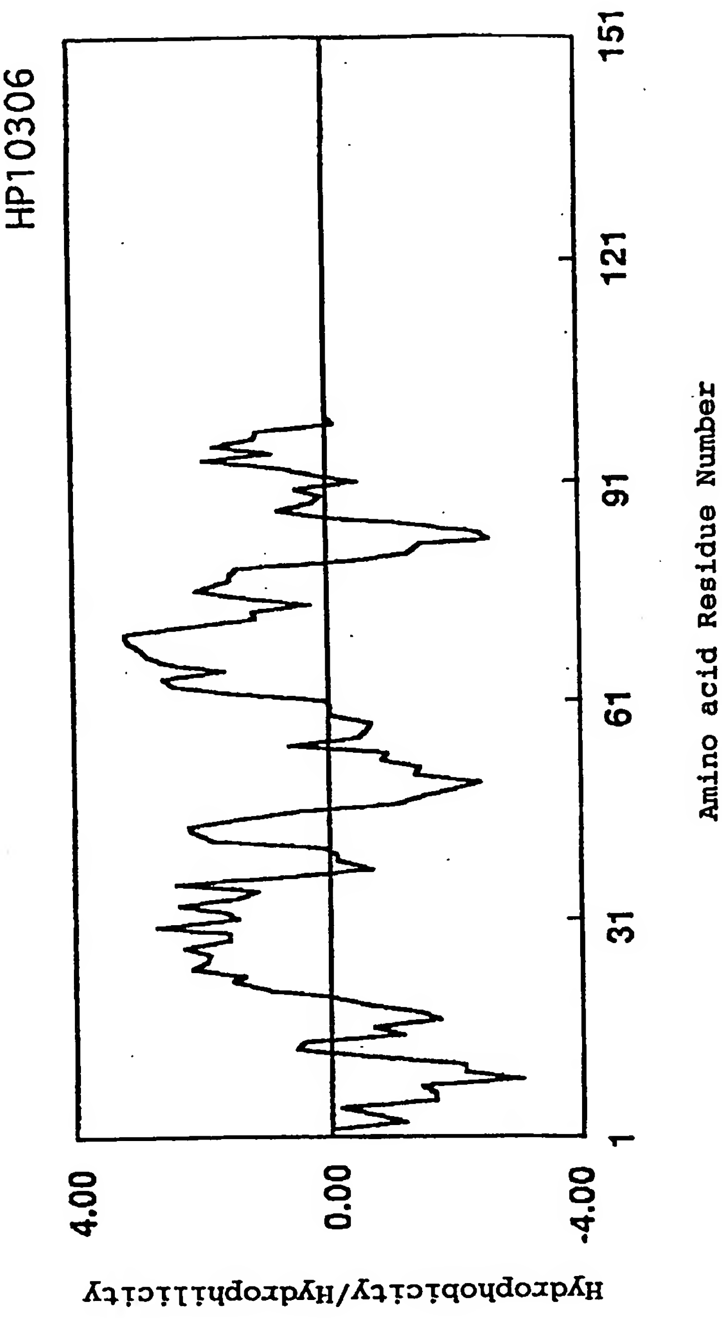
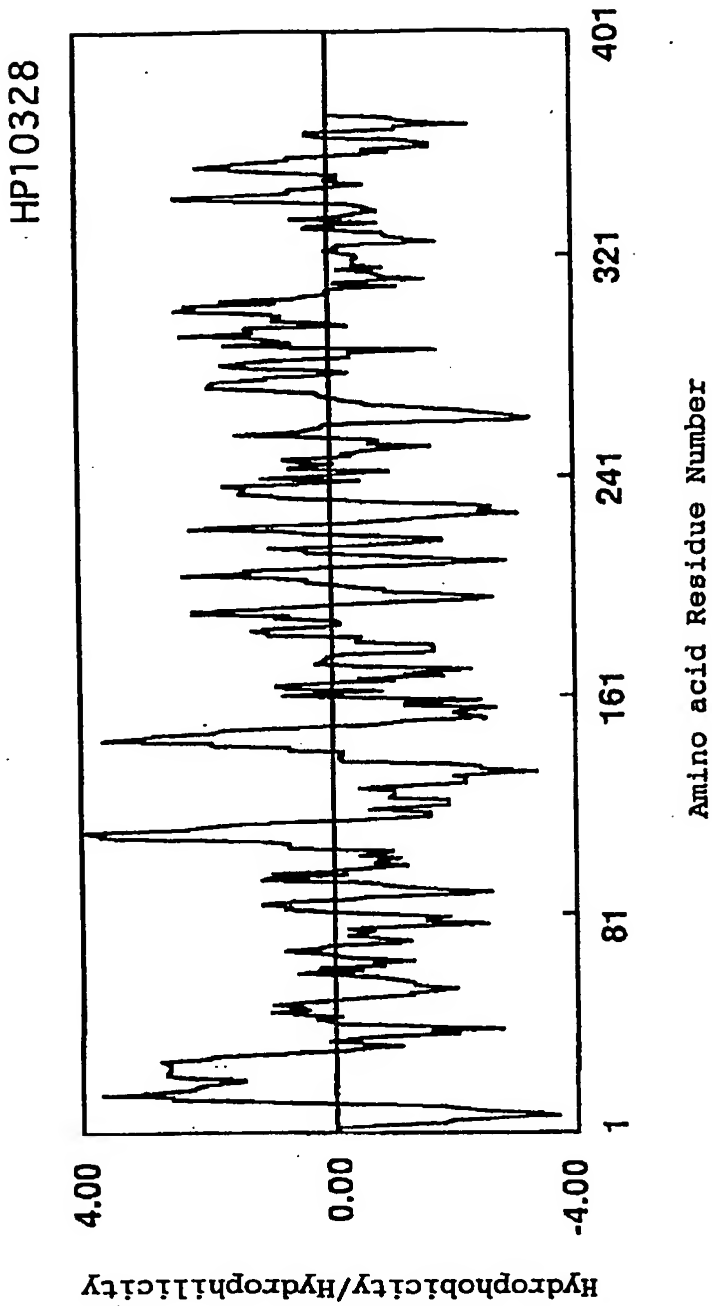

HP10306
4.00
0.00
-4.00
Hydrophobicity/Hydrophilicity
1
31
61
91
121
151
Amino acid Residue Number

Fig. 28


HP10328
4.00
0.00
-4.00
Hydrophobicity/Hydrophilicity
1
81
161
241
321
401
Amino acid Residue Number